



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number 119788

TO: Olga Chernyshev
Location: rem 4e84 & 4c70
Art Unit: 1646
Wednesday, April 21, 2004

Case Serial Number: 09/919473

From: Toby Port
Location: Biotech-Chem Library
Remsen 1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Chernyshev,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 20, 2004, 18:51:47 ; Search time 18.24 Seconds
(without alignments)
657.330 Million cell updates/sec

Title: US-09-919-473-11

Perfect score: 179
Sequence: 1 VILSDVPITGLIRILEQARYKAAEQAAATNAQILAHV 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriopl:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	49.2	151	13 Q918B5	Q918B5 fugu rubrip
2	60	33.5	42	6 O77577	O77577 ovis aries
3	60	33.5	209	11 Q9DC90	Q9DC90 mus musculu
4	57	31.8	165	13 Q7ZZM1	Q7ZZM1 spea hammon
5	57	31.8	187	11 Q8CITO	Q8CITO mus musculu
6	57	31.8	191	6 Q8HZV1	Q8HZV1 sus scrofa
7	56	31.3	162	13 Q8UHU6	Q8UHU6 cyprinus ca
8	56	31.3	1795	4 Q9E2B8	Q9E2B8 homo sapien
9	53.5	29.9	270	3 Q9F781	Q9F781 schizosach
10	53	29.6	69	6 O77778	O77778 ovis aries
11	53	29.6	279	2 Q8KZRS	Q8KZRS pseudomonas
12	53	29.6	279	16 Q88RA2	Q88RA2 pseudomonas
13	53	29.6	417	16 Q9BLJ7	Q9BLJ7 thizobium 1
14	52.5	29.3	492	16 Q88XRO	Q88XRO pseudomonas
15	52.5	29.3	802	5 Q88Z78	Q88Z78 drosophila
16	52	29.1	161	13 Q7ZZU9	Q7ZZU9 ameleturus ne

17	52	29.1	166	13 Q800D2	Q800D2 salvelinus
18	52	29.1	167	13 Q919D0	Q919D0 oreochromis
19	52	29.1	167	13 Q7SKA4	Q7SKA4 oncorhynch
20	52	29.1	248	2 Q7X390	Q7X390 escherichia
21	52	29.1	393	10 Q49567	Q49567 arabidopsis
22	52	29.1	399	5 Q8SWJ8	Q8SWJ8 encphallito
23	52	29.1	494	16 Q7VSM0	Q7VSM0 bordetella
24	52	29.1	500	16 Q7WFS1	Q7WFS1 bordetella
25	52	29.1	500	16 Q7W3S3	Q7W3S3 bordetella
26	52	29.1	514	5 Q8VXU5	Q8VXU5 drosophila
27	52	29.1	1064	5 Q65UL0	Q65UL0 caenorhadi
28	52	29.1	1275	5 Q9Y1H5	Q9Y1H5 dictyostell
29	51.5	28.8	464	2 Q93J78	Q93J78 pseudomonas
30	51	28.5	220	16 Q88ZY1	Q88ZY1 lactobacill
31	51	28.5	412	16 Q9A254	Q9A254 caulobacter
32	51	28.5	817	10 Q7XSF1	Q7XSF1 cryza sativ
33	50.5	28.2	1093	10 Q84M30	Q84M30 arabidopsis
34	50.5	28.2	1325	10 Q64533	Q64533 arabidopsis
35	50	27.9	159	16 Q92D25	Q92D25 listeria in
36	50	27.9	343	16 Q7USE1	Q7USE1 rhodospirell
37	50	27.9	416	13 Q9DD52	Q9DD52 brachydanio
38	50	27.9	419	16 Q8UCR4	Q8UCR4 agrobacteri
39	50	27.9	485	16 Q88T41	Q88T41 lactobacill
40	50	27.9	523	10 Q7XEM4	Q7XEM4 cryza sativ
41	50	27.9	1065	16 Q81BP4	Q81BP4 bacillus ce
42	50	27.9	1082	5 Q9SU36	Q9SU36 drosophila
43	50	27.9	1325	5 Q9VP80	Q9VP80 drosophila
44	50	27.9	1887	12 Q9IMS9	Q9IMS9 cherry moult
45	49.5	27.7	105	16 Q9CUE7	Q9CUE7 pasteurrella

ALIGNMENTS

RESULT 1

Q918B5 PRELIMINARY; PRT; 151 AA.

AC Q918B5; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2000 (TREMBLrel. 19, Last annotation update)
DE Urococtin precursor.
GN UCN.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=11033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20485066; PubMed=11032317;
RA Brunner B., Gruetzer F., Yaspo M.U., Ropers H.H., Haaf T.,
RA Kalscheuer V.M.;
RT "Molecular cloning and characterization of the Fugu rubripes
RT MSTR/COP2 imprinting cluster and chromosomal localization in Fugu and
RT Tetraodon nigroviridis";
RL Chromosome Res. 8:465-476 (2000).
FT EMBL; AJ251323; CAB96535.1; -.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 151 AA; 16686 MW; EEBID52C41A67124 CRC64;

Query Match 49.2%; Score 88; DB 13; Length 151;

Best Local Similarity 47.2%; Pred. No. 4.5e-05;

Matches 17; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

RESULT 2

077577 PRELIMINARY; PRT; 42 AA.
 ID 077577;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DT UROCOCTIN precursor (Fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Caprinae; Ovis.
 OC NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cepot D., Sutton S., Vale W.W.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RP [12]
 RP SEQUENCE OF 14-42 FROM N.A.
 RA Baigent S.M., Lowy P.J.;
 RT "The cloning of ovine urocortin."
 RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF051807; AAC27288.1; -
 DR EMBL; AF084258; AAC33478.1; -
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR InterPro; IPR00187; corticoliberin.
 DR InterPro; IPR003620; Urocortin_CRF.
 DR Pfam; PF00473; CRF; 1.
 DR PRINTS; PRO1612; CRFFAMILY.
 DR SMART; SM00039; CRF; 1.
 DR PROSITE; PS00511; CRF; 1.
 FT NON TER 1 1
 FT NON TER 1 1
 SQ SEQUENCE 42 AA; 4893 MW; 31D6139D4937C9E2 CRC64;
 Query Match 33.5%; Score 60; DB 6; Length 42;
 Best Local Similarity 44.4%; Pred. No. 0.17;
 Matches 16; Conservative 5; Mismatches 15; Indels 0; Gaps 0;
 QY 3 LSLDVPGLIRILLLEQARYKARNOATNAQILAHV 38
 DB 5 LSLDTFHLRLTLLEARTQSCREARERKNRIIPDSV 40
 RESULT 3
 ID 09DC90 PRELIMINARY; PRT; 209 AA.
 AC 09DC90;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DT Preproprotein convertase subtilisin/kexin type 4.
 GN PCSK4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Scurionath; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=CS7BL/6J; TISSUE=Brain;
 RC MEDLINE=21085660; PubMed=11217851;
 RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 Arai K., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 Aikawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 Schirini L.W., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Baren G.,
 Blake J., Bokfield D., Bojunga N., Carninci P., de Bonaldo M.F.,
 Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 Gattung S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilting L.,
 Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL; AK003053; BAB22535.1; -
 DR MED; MG1:97514; Pcc4.
 SQ SEQUENCE 209 AA; 22636 MW; 3ACFC611907DD17D CRC64;
 Query Match 33.5%; Score 60; DB 11; Length 209;
 Best Local Similarity 50.0%; Pred. No. 1.1;
 Matches 12; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 QY 8 PIGLLRILLLEQARYKARNOATN 31
 DB 98 PIGLRKHLPPARYPSKONHACTD 121
 RESULT 4
 ID 07Z2M1 PRELIMINARY; PRT; 165 AA.
 AC 07Z2M1;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Corticotropin-releasing hormone precursor.
 OS Spina hamondii (western spadefoot toad).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pelobatoidae; Pelobatidae;
 OC Spee.
 OC NCBI_TaxID=228670;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=Brain;
 RA Boorse G.C., Denver R.J.;
 RT "Endocrine mechanisms underlying plasticity in metamorphic timing in
 spadefoot toads."
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY262255; AAP20883.1; -
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR InterPro; IPR00187; corticoliberin.
 DR InterPro; IPR003620; Urocortin_CRF.
 DR Pfam; PF00473; CRF; 1.
 DR PRINTS; PRO1612; CRFFAMILY.
 DR PRODOM; PD005970; Urocortin_CRF; 1.
 DR SMART; SM00039; CRF; 1.
 DR PROSITE; PS00511; CRF; 1.
 KW Signal.
 FT CHAIN 1 24 Potential.
 FT CHAIN 123 163 corticotropin-releasing hormone.
 SQ SEQUENCE 165 AA; 18443 MW; D7A3BF5BC810E94 CRC64;
 Query Match 31.8%; Score 57; DB 13; Length 165;
 Best Local Similarity 39.4%; Pred. No. 2.3;
 Matches 13; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
 QY 3 LSLDVPGLIRILLLEQARYKARNOATNAQIL 35
 DB 128 LSLDTFHLRLTLLEQARYKARNOATNAQIL 160
 RESULT 5
 ID 08CIT0 PRELIMINARY; PRT; 187 AA.
 AC 08CIT0;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Preprocorticotropin-releasing hormone.

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Seasholtz A.F., Bourbonnais F.J., Harnden C.E., Camper S.A.;
RT "Nucleotide Sequence and Expression of the Mouse Corticotropin-
  Releasing Hormone Gene.";
RL Mol. Cell. Neurosci. 2:266-273 (1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Seasholtz A.F., Bourbonnais F.J., Harnden C.E., Camper S.A.;
RL EMBL; AY128673; AAN07905.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR000187; corticoliberin.
DR Pfam; PF00473; CRF; 1.
DR PRINTS; PR01612; CRPFAMILY.
DR PRODOM; PD005970; Urocortin_CRF; 1.
DR SMART; SM00039; CRF; 1.
DR PROSITE; PS00511; CRF; 1.
FT CHAIN 145 187
SQ SEQUENCE 187 AA; 20778 MW; 5851665291FAA998 CRC64;

Query March 31.8%; Score 57; DB 11; Length 187;
Best Local Similarity 39.4%; Pred. No. 2.7;
Matches 13; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 3 LSLDVPGLRLLEQARYKARNQATNAQIL 35
Db 150 ISLDLTFHLRLVLEWRAAEQLAQAHNRKLM 182

RESULT 6
Q8HZV1 PRELIMINARY; PRT; 191 AA.
AC Q8HZV1;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Corticotropin releasing hormone.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
CX NCBI_TaxID=96823;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22027062; PubMed=12030933;
RA Wimmers K., Mourati E., Fomuskis S., Schellander K.;
RT "Sequence variation and linkage mapping of the porcine corticotropin
  releasing hormone (CRH) gene.";
RL Anim. Genet. 33:233-234 (2002).
DR EMBL; AF440229; AAN0888.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR000187; corticoliberin.
DR InterPro; IPR003620; Urocortin_CRF.
DR Pfam; PF00473; CRF; 1.
DR PRINTS; PR01612; CRPFAMILY.
DR PRODOM; PD005970; Urocortin_CRF; 1.
DR SMART; SM00039; CRF; 1.
DR PROSITE; PS00511; CRF; 1.
SQ SEQUENCE 191 AA; 20969 MW; 507950F0A0AC9011 CRC64;

Query March 31.8%; Score 57; DB 6; Length 191;
Best Local Similarity 39.4%; Pred. No. 2.8;
Matches 13; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

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QY 3 LSLDVPGLRLLEQARYKARNQATNAQIL 35
Db 154 ISLDLTFHLRLVLEWRAAEQLAQAHNRKLM 186

RESULT 7
Q8UHU6 PRELIMINARY; PRT; 162 AA.
AC Q8UHU6;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Putative corticotropin releasing hormone precursor.
GN CRH.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
CX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Macrophage;
RA Huisling M.O., van den Burg E.H., Verburg-van Kemenade L.B.M., Flik G.;
RT "Expression of corticotropin releasing hormone (CRH) in the common
  carp (Cyprinus carpio L.).";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ317935; CAC84859.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR000187; corticoliberin.
DR InterPro; IPR003620; Urocortin_CRF.
DR Pfam; PF00473; CRF; 1.
DR PRINTS; PR01612; CRPFAMILY.
DR SMART; SM00039; CRF; 1.
DR PROSITE; PS00511; CRF; 1.
FT SIGNAL 120 160
FT CHAIN 1 119
SQ SEQUENCE 162 AA; 18300 MW; 511DDBA0D1E2A5C9 CRC64;

Query March 31.3%; Score 56; DB 13; Length 162;
Best Local Similarity 39.4%; Pred. No. 3.2;
Matches 13; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 3 LSLDVPGLRLLEQARYKARNQATNAQIL 35
Db 125 ISLDLTFHLRLVLEWRAAEQLAQAHNRKLM 157

RESULT 8
Q9P2B8 PRELIMINARY; PRT; 1795 AA.
AC Q9P2B8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein KIAA1429 (Fragment).
GN KIAA1429.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=20181126; PubMed=10718198;
RA Nagase T., Kikuno R., Ishikawa K., Hirosewa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes XVI.
  The complete sequences of 150 new cDNA clones from brain which code
  for large proteins in vitro.";
RL DNA Res. 7:65-73 (2000).
DR EMBL; AB037850; BAA92667.1; -
DR GO; GO:0003676; F:nucleic acid binding; IEA.

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DR INTERPRO; IPR000504; RNA_rec.mot.
DR PROSITE; PS00030; RRM_RNP_1; 1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 1795 AA; 200853 MW; B26CDB49A6961063 CRC64;

Query Match 31.3%; Score 56; DB 4; Length 1795;
Best Local Similarity 34.4%; Pred. No. 52;
Matches 11; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

Qy 6 DVPIGLRLLEQARYKARNQATNAQILAH 37
Db 1684 EAPVGVRLLEELTETKVEARALTEALFHH 1715

RESULT 9
Q9P781 PRELIMINARY; PRT; 270 AA.
AC Q9P781;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Hypothetical protein.
GN SPBC1711.09C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OC NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972h-.
RA Aert R., Voiclaert G., Wood V., Rajandream M.A., Barrell B.G.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; A1531012; CAB88239.1; -.
DR GeneDB; Spombe; SPBC1711.09c; -.
KW Hypothetical protein.
SQ SEQUENCE 270 AA; 30067 MW; 0316EA38FEC30D37 CRC64;

Query Match 29.9%; Score 53.5; DB 3; Length 270;
Best Local Similarity 34.9%; Pred. No. 14;
Matches 15; Conservative 11; Mismatches 10; Indels 7; Gaps 3;

Qy 1 VILSDVPIGLRLLEQARYKARNQATNAQILAH 38
Db 195 IYLVIPALATATGTRVDPATRAAGSGATKALIHV 235

RESULT 10
Q77778 PRELIMINARY; PRT; 69 AA.
AC Q77778;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Urococtin (Pragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Richardson M.P.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF085534; AAC35555.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR000187; Corticosteroid.
DR InterPro; IPR001620; Urococtin_CRF.
DR Pfam; PF00473; CRF; 1.
DR PRINTS; PR01612; CRPFAM11.
DR SMART; SM00039; CRF; 1.
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DR PROSITE; PS00511; CRF; 1.
FT NON_TER 1
FT NON_TER 69
SQ SEQUENCE 69 AA; 8132 MW; E437469148BC219A CRC64;

Query Match 29.6%; Score 53; DB 6; Length 69;
Best Local Similarity 44.8%; Pred. No. 3.4;
Matches 13; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 3 LSLDVPGLRLLEQARYKARNQATNAQILAH 31
Db 37 LSLDLPFLRLLELARTSQXERAEON 65

RESULT 11
Q8KZRS PRELIMINARY; PRT; 279 AA.
AC Q8KZRS;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE ABC-type transporter membrane permease component.
GN TAUC.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OC NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DS1;
RA Endoh T., Kasuga K., Horiouchi M., Yoshida T., Habe H., Nojiri H.,
RA Omori T.;
RL "Characterization and identification of genes essential for dimethyl
RT sulfide-utilization in Pseudomonas putida strain DS1."
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM.
CC PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF THE SUBSTRATE ACROSS
CC THE MEMBRANE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT
CC SYSTEM PERMEASE FAMILY.
DR EMBL; AB086390; BAC00966.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000515; BPD_transp.
DR Pfam; PF00528; BPD_transp; 1.
DR PROSITE; PS00402; BPD_TRANS_P_NN_MEMBER; 1.
KW Transmembrane; Transport.
SQ SEQUENCE 279 AA; 29760 MW; 42FE5664C8133719 CRC64;

Query Match 29.6%; Score 53; DB 2; Length 279;
Best Local Similarity 28.6%; Pred. No. 17;
Matches 12; Conservative 12; Mismatches 14; Indels 4; Gaps 1;

Qy 1 VILSDVPIGLRLLEQARYKARNQATNAQILAH 38
Db 153 IYLVIPALATATGTRVDPATRAAGSGATKALIHV 194

RESULT 12
Q88RA2 PRELIMINARY; PRT; 279 AA.
AC Q88RA2;
DT 01-JUN-2003 (TREMblrel. 24, Created)
DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Taurine ABC transporter, permease protein.
GN TAUC OR PF0231.
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OC NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
```


RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RA Stapleton M., Brokstein P., Hong L., Agbayan A., Carlson J.,
 RA Change M., Chavez C., Dorsett V., Drensek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda M., Mungall C.J., Nuno U., Paclab V., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Gabow G.L.,
 RA Abril J.F., Agbayani A., An H.U., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu U., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertan B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck U., Brokstein P., Brotlier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Ke Z., Kennison J.G., Ketchum K.A.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Meinhart M., Idegian C.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasok P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclab J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Splet B., Spradling A.C., Stapleton M., Strong R., Sun B.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissendach J.,
 RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RL "The genome sequence of *Drosophila melanogaster*.";
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celniker S.E.,
 RA Clamp W.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J.,
 RA Harris N.L., Krommiller B., Marshall B., Millburn G.H., Richter J.,
 RA Russo S., Searle S.M.J., Smith E., Shu S., Smutnak F.,
 RA Whitfield E.J., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J.,
 RA Lewis S.E.;
 RL "Annotation of *Drosophila melanogaster* genome.";
 RN [4]
 RP Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 RN EMBL; AY071063; AA148685.1; -;
 DR EMBL; AB003776; AAF57115.2; -;

DR FlyBase; FBgn0039818; CG11318.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004930; F:g-protein coupled receptor activity; IEA.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR000203; PKD_Cys_rich.
 DR Pfam; PF00002; 7tm_2_1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR PROSITE; PS50221; GPS; 1.
 DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
 SQ SEQUENCE 802 AA; 90457 MW; D6382D4F5DB521D CRC64;

Query Match 29.3%; Score 52.5; DB 5; Length 802;
 Best Local Similarity 41.7%; Pred. No. 69;
 Matches 15; Conservative 9; Mismatches 7; Indels 5; Gaps 2;

Qy 3 LSLDPVPLGLRILIEQARYTAPRNOATNAQIIAHV 38
 Db 511 LSL---LGIIGIFLTAFLFKMRSQAST--KVLHL 541

Search completed: April 20, 2004, 18:56:44
 Job time : 20.24 secs

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: April 20, 2004, 18:51:32 ; Search time 5.06667 Seconds
(without alignments)
390.526 Million cell updates/sec

Title: US-09-919-473-11

Perfect score: 179
Sequence: 1 VILSIDVPIGLRLILEQARYKARNQATNAQIIAHV 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	179	100.0	112	1	UCN2_MOUSE
2	162	90.5	109	1	UCN2_MOUSE
3	139	77.7	112	1	UCN2_MOUSE
4	78	43.6	161	1	UCN3_HUMAN
5	75	41.9	164	1	UCN3_MOUSE
6	61	34.1	41	1	UCN1_MOUSE
7	60	33.5	122	1	UCN1_MOUSE
8	60	33.5	122	1	UCN1_MOUSE
9	60	33.5	124	1	UCN1_MOUSE
10	60	33.5	145	1	UCN1_MOUSE
11	60	33.5	145	1	UCN1_MOUSE
12	60	33.5	165	1	UCN1_MOUSE
13	57	31.8	162	1	UCN1_MOUSE
14	57	31.8	162	1	UCN1_MOUSE
15	57	31.8	162	1	UCN1_MOUSE
16	57	31.8	162	1	UCN1_MOUSE
17	56	31.3	162	1	UCN1_MOUSE
18	56	31.3	162	1	UCN1_MOUSE
19	54	30.2	162	1	UCN1_MOUSE
20	54	30.2	162	1	UCN1_MOUSE
21	53	29.6	162	1	UCN1_MOUSE
22	50	27.9	190	1	UCN1_MOUSE
23	50	27.9	190	1	UCN1_MOUSE
24	49.5	27.7	633	1	UCN1_MOUSE
25	49.5	27.7	633	1	UCN1_MOUSE
26	49.5	27.7	633	1	UCN1_MOUSE
27	48.5	27.1	901	1	UCN1_MOUSE
28	48.5	27.1	901	1	UCN1_MOUSE
29	48.5	27.1	901	1	UCN1_MOUSE
30	48.5	27.1	901	1	UCN1_MOUSE
31	48.5	27.1	901	1	UCN1_MOUSE
32	48.5	27.1	901	1	UCN1_MOUSE
33	48.5	27.1	901	1	UCN1_MOUSE

ALIGNMENTS

Result ID	Query Match	Length	ID	Description
1	100.0	112	1	UCN2_MOUSE
2	90.5	109	1	UCN2_MOUSE
3	77.7	112	1	UCN2_MOUSE
4	43.6	161	1	UCN3_HUMAN
5	41.9	164	1	UCN3_MOUSE
6	34.1	41	1	UCN1_MOUSE
7	33.5	122	1	UCN1_MOUSE
8	33.5	122	1	UCN1_MOUSE
9	33.5	124	1	UCN1_MOUSE
10	33.5	145	1	UCN1_MOUSE
11	33.5	145	1	UCN1_MOUSE
12	33.5	165	1	UCN1_MOUSE
13	31.8	162	1	UCN1_MOUSE
14	31.8	162	1	UCN1_MOUSE
15	31.8	162	1	UCN1_MOUSE
16	31.8	162	1	UCN1_MOUSE
17	31.3	162	1	UCN1_MOUSE
18	31.3	162	1	UCN1_MOUSE
19	30.2	162	1	UCN1_MOUSE
20	30.2	162	1	UCN1_MOUSE
21	29.6	162	1	UCN1_MOUSE
22	27.9	190	1	UCN1_MOUSE
23	27.9	190	1	UCN1_MOUSE
24	27.7	633	1	UCN1_MOUSE
25	27.7	633	1	UCN1_MOUSE
26	27.7	633	1	UCN1_MOUSE
27	27.1	901	1	UCN1_MOUSE
28	27.1	901	1	UCN1_MOUSE
29	27.1	901	1	UCN1_MOUSE
30	27.1	901	1	UCN1_MOUSE
31	27.1	901	1	UCN1_MOUSE
32	27.1	901	1	UCN1_MOUSE
33	27.1	901	1	UCN1_MOUSE

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VILSDVPIGLRLILBQARYKAAKRNQATNQAIIAHV 38
DB 72 VILSDVPIGLRLILBQARYKAAKRNQATNQAIIAHV 109

RESULT 2
UCN2_RAT STANDARD; PRT: 109 AA.

DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DR Urocortin II precursor (Ucn II).
GN UCN2.
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Midbrain;
RA Park J.H., Ju S.K., Lee M.K.;
RT "Cloning and analysis of tissue-specific mRNA expression of rat
RT urocortin II.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Suppresses food intake, delays gastric emptying and
CC decreases heat-induced edema. Might represent an endogenous ligand
CC for maintaining homeostasis after stress (By similarity).
CC -1- SUBUNIT: Binds with high affinity to CRF receptors 2-alpha and 2-
CC beta (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC factor/urotensin I family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AY044835; AAK98780.1; -
DR GO: GO:0005576; C:extracellular; ISS.
DR GO: GO:0005102; P:receptor binding; ISS.
DR GO: GO:0006171; P:cAMP biosynthesis; ISS.
DR GO: GO:0007586; P:digestion; ISS.
DR GO: GO:0006950; P:response to stress; ISS.
DR InterPro: IPR000187; corticotiberin.
DR SMART: SM00039; CRF; 1.
KW Hormone; Amidation; Signal.
FT SIGNAL 19
FT PROPEP 20
FT CHAIN 69 109
FT SEQUENCE 109 AA; 11922 MW; AAZB46D8903ED83E CRC64;

Query Match 90.5%; Score 162; DB 1; Length 109;
Best Local Similarity 94.7%; Pred. No. 1.8e-16;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VILSDVPIGLRLILBQARYKAAKRNQATNQAIIAHV 38
DB 69 VILSDVPIGLRLILBQARYKAAKRNQATNQAIIAHV 106

RESULT 3
UCN2_HUMAN STANDARD; PRT: 112 AA.

AC 096RE3; 09BUC0; (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Urocortin II precursor (Ucn II) (stresscopin-related peptide)
DE (Urocortin-related peptide).
GN UCN2 OR SRP OR URP.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21227098; PubMed=11329063;
RA Heu S.Y., Hsueh A.J.W.;
RT "Human stresscopin and stresscopin-related peptide are selective
RT ligands for the type 2 corticotropin-releasing hormone receptor";
RL Nat. Med. 7:605-611(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin, and Uterus;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., Wehman P., McKernan K.J., Malek J.A., Gamarate P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Munhy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smalins D.E.,
RA Schmeich A., Schein J.E., Jones S.J.M., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Suppresses food intake, delays gastric emptying and
CC decreases heat-induced edema. Might represent an endogenous ligand
CC for maintaining homeostasis after stress.
CC -1- SUBUNIT: Binds with high affinity to CRF receptors 2-alpha and 2-
CC beta.
CC
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC factor/urotensin I family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF320560; AAK52672.1; -
DR EMBL: BC002647; AAH02647.2; -
DR EMBL: BC022096; AAH22096.1; -
DR MIM: 605902; -
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0005102; P:receptor binding; IPT.
DR GO: GO:0006171; P:cAMP biosynthesis; IEP.
DR GO: GO:0007586; P:digestion; NAS.
DR GO: GO:0006950; P:response to stress; NAS.
DR InterPro: IPR000187; corticotiberin.
DR SMART: SM00039; CRF; 1.
KW Hormone; Amidation; Signal.
FT SIGNAL 19
FT PROPEP 20
FT CHAIN 72 112
FT SEQUENCE 112 AA; 12146 MW; 0EF29A3463723D4 CRC64;

DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Urotensin I.
 OS Catestomus commersoni (White sucker).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Catestomidae; Catestomus.
 OX NCBI_TaxID=7971;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=8301606; PubMed=6981844;
 RA Lederis K., Letter A., McMaster D., Moore G., Schlesinger D.;
 RT "Complete amino acid sequence of urotensin I, a hypotensive and
 RT corticotropin-releasing neuropeptide from Catestomus.";
 RL Science 218:162-164(1982).
 CC [2]
 RP SEQUENCE.
 RX MEDLINE=84025881; PubMed=6313156;
 RA Lederis K., Letter A., McMaster D., Ichikawa T., McCannell K.L.,
 RA Rivier J., Rivier C., Vale W., Fryer J., Kobayashi Y.;
 RT "Isolation, analysis of structure, synthesis, and biological actions
 RT of urotensin I neuropeptides.";
 RL Can. J. Biochem. Cell Biol. 61:602-614(1983).
 CC -1- FUNCTION: Urotensin is found in the teleost caudal neurosecretory
 CC system. It has a suggested role in osmoregulation and as a
 CC corticotropin-releasing factor.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC factor/urotensin I family.
 CC PIR, A94267; UOCCIM.
 CC InterPro: IPR000187; corticoliberin.
 CC InterPro: IPR003620; Urocortin_CRF.
 CC Pfam: PF00473; CRF; 1.
 CC PRINTS: PR01612; CRFFAMILY.
 CC ProDom: PD005970; Urocortin_CRF; 1.
 CC SMART: SM00039; CRF; 1.
 CC PROSITE: PS00511; CRF; 1.
 CC Hormone; Amidation.
 CC MOD_RES 41
 CC MOD_RES 41
 CC SEQUENCE 41 AA; 4870 MW; AAE309BFA1971 CRC64;
 SQ
 Query Match 34.1%; Score 61; DB 1; Length 41;
 Best Local Similarity 38.9%; Pred. No. 0.03;
 Matches 14; Conservative 7; Mismatches 15; Indels 0; Gaps 0;
 QY 3 LSLDVPGLRLLEQARYKAARNOATNAQILAHV 38
 DB 6 ISLDLTFHLRLNMIEMARIENEREQGLNRKYLDV 41
 RESULT 7
 UCNT_MOUSE STANDARD; PRT; 122 AA.
 ID UCNT_MOUSE
 AC P81615; O88390;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Urocortin precursor.
 GN UCN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98282491; PubMed=9628819;
 RA Zhao L., Donaldson C.J., Smith G.W., Vale W.W.;
 RT "The structures of the mouse and human urocortin genes.";
 RL Genomics 50:23-33(1998).
 CC -1- FUNCTION: Acts in vitro to stimulate the secretion of
 CC adrenocorticotrophic hormone (ACTH). Binds with high affinity to
 CC CRF Receptor types 1, 2-alpha, and 2-beta.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC factor/urotensin I family.
 CC -1- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing

CC factor/urotensin I family.
 CC -----
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 CC -----
 CC EMBL AF038632; AAC24202.1; ..
 CC MGD; MGI:1276123; Ucn.
 CC InterPro: IPR000187; corticoliberin.
 CC InterPro: IPR003620; Urocortin_CRF.
 CC Pfam: PF00473; CRF; 1.
 CC PRINTS: PR01612; CRFFAMILY.
 CC SMART: SM00039; CRF; 1.
 CC PROSITE: PS00511; CRF; 1.
 CC Hormone; Amidation; Cleavage on pair of basic residues; Signal.
 CC SIGNAL 1
 CC PROPEP 26 80
 CC PEPIDE 81 120
 CC MOD_RES 120 120
 CC SEQUENCE 122 AA; 13557 MW; D2969756F36F5DEA CRC64;
 SQ
 Query Match 33.5%; Score 60; DB 1; Length 122;
 Best Local Similarity 44.4%; Pred. No. 0.13;
 Matches 16; Conservative 5; Mismatches 15; Indels 0; Gaps 0;
 QY 3 LSLDVPGLRLLEQARYKAARNOATNAQILAHV 38
 DB 85 LSLDLPFLRLLELARTOSQREARLQNRNIPDSV 120
 RESULT 8
 UCNT_RAT STANDARD; PRT; 122 AA.
 ID UCNT_RAT
 AC P55090;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Urocortin precursor (corticotensin).
 GN UCN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=96065764; PubMed=7477349;
 RA Vaughan J.M., Donaldson C.J., Biltencourt J., Perrin M.H., Lewis K.A.,
 RA Sutton S.W., Chan R., Turnbull A., Lovejoy D., Rivier C., Rivier J.E.,
 RA Sawchenko P., Vale W.W.;
 RT "Urocortin, a mammalian neuropeptide related to fish urotensin I and
 RT to corticotropin-releasing factor.";
 RL Nature 378:287-292(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Lewis;
 RA PARK J.H., Lee Y.J., Kim K.L.;
 RT "Detection of rat urocortin in lymphoid tissues: implications for the
 RT functional assessment of urocortin as a novel neuro-immunomodulatory
 RT peptide.";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Acts in vitro to stimulate the secretion of
 CC adrenocorticotrophic hormone (ACTH). Binds with high affinity to
 CC CRF Receptor types 1, 2-alpha, and 2-beta.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC factor/urotensin I family.
 CC -----

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CC or send an email to license@isb-sib.ch).

DR EMBL; U39355; AAA87566.1; -
DR EMBL; AF093623; AAF63153.1; -
DR PIR; S60262; S60262.
DR InterPro; IPR00187; corticotiberin.
DR InterPro; IPR003620; Urocortin_CRF.
DR Pfam; PF00473; CRF; 1.
DR PRINTS; PRO1612; CRFPAMLY.
DR SMART; SMO0039; CRF; 1.
DR PROSITE; PS00511; CRF; 1.
DR Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT PROPEP 26 80
FT PEPTIDE 81 120 UROCORTIN.
FT MOD_RES 120 120 AMIDATION (G-121 PROVIDE AMIDE GROUP) (BY
SIMILARITY).
SQ SEQUENCE 122 AA; 13711 MW; 9F0AF834CBFC74 CRC64;

Query Match 33.5%; Score 60; DB 1; Length 122;
Best Local Similarity 44.4%; Pred. No. 0.13;
Matches 16; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 3 LSLDVPGLRLTLLEQARYKKAARNQATNAQILAHV 38
DB 85 LSLDLPFLRLTLLELARTQSGRRERAEQNRIIFDSV 120

RESULT 9
UCN1 HUMAN STANDARD; PRT; 124 AA.
AC P55089;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Urocortin precursor.
GN UCN1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA MEDLINE=96198824; PubMed=8612563;
RA Donaldson C.J., Sutton S.W., Perrin M.H., Corrigan A.Z., Lewis K.A.,
RA Rivier J.B., Vaughan J.M., Vale W.W.;
RA "Cloning and characterization of human urocortin."
RA Endocrinology 137:2167-2170(1996).

RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98292491; PubMed=9628819;
RX Zhao L., Donaldson C.J., Smith G.W., Vale W.W.;
RT "The structures of the mouse and human urocortin genes."
RT Genomics 50:33-33(1998).
CC -1- FUNCTION: Acts in vitro to stimulate the secretion of
CC adrenocorticotrophic hormone (ACTH). Binds with high affinity to
CC CRF receptor types 1, 2-alpha, and 2-beta.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC factor/urocortin I family.

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DR EMBL; AF038633; AAC24204.1; -
DR Genew; HGNC:12516; UCN.
DR MIM; 600945;
DR GO; GO:0005184; F:neuropeptide hormone activity; TAS.
DR GO; GO:0007186; F:G-protein coupled receptor protein signaln. .; TAS.
DR InterPro; IPR00187; corticotiberin.
DR InterPro; IPR003620; Urocortin_CRF.
DR Pfam; PF00473; CRF; 1.
DR PRINTS; PRO1612; CRFPAMLY.
DR SMART; SMO0039; CRF; 1.
DR PROSITE; PS00511; CRF; 1.
DR Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT PROPEP 26 82
FT PEPTIDE 83 122 UROCORTIN.
FT MOD_RES 122 122 AMIDATION (G-123 PROVIDE AMIDE GROUP) (BY
SIMILARITY).
SQ SEQUENCE 124 AA; 13458 MW; 4F765DA75BDD4A5E CRC64;

Query Match 33.5%; Score 60; DB 1; Length 124;
Best Local Similarity 44.4%; Pred. No. 0.13;
Matches 16; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 3 LSLDVPGLRLTLLEQARYKKAARNQATNAQILAHV 38
DB 87 LSLDLPFLRLTLLELARTQSGRRERAEQNRIIFDSV 122

RESULT 10
URL CARAU STANDARD; PRT; 145 AA.
ID Q9PT04;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Urocortin I precursor.
DE Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20072640; PubMed=10603283;
RX Bernier N.U., Lin X., Peter R.E.;
RT "Differential expression of corticotropin-releasing factor (CRF) and
RT urocortin I precursor genes, and evidence of CRF gene expression
RT regulated by cortisone in goldfish brain."
RT Gen. Comp. Endocrinol. 116:461-477(1999).
CC -1- FUNCTION: Urocortin is found in the telost caudal neurosecretory
CC system. It has a suggested role in homeostatic regulation and as a
CC corticotropin-releasing factor. The nonhomologous portion of this
CC precursor may be a urocortin binding protein, urophysin.

CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC factor/urocortin I family.
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DR EMBL; AF129115; AAF24136.1; -
DR InterPro; IPR00187; corticotiberin.
DR InterPro; IPR003620; Urocortin_CRF.
DR Pfam; PF00473; CRF; 1.


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DR PRINTS; PRO1612; CRPFAMILY.
DR PRODOM; PD005970; Urocortin_CRF; 1.
DR SMART; SM00039; CRF; 1.
DR PROSITE; PS00511; CRF; 1.
DR Hormone; Cleavage on pair of basic residues; Amidation; Signal.
KW SIGNAL
FT CHAIN 1 22
FT PEPTIDE 103 143 UROPHYSIN I. (POTENTIAL).
FT MOD_RES 143 143 AMIDATION (G-144 PROVIDE AMIDE GROUP) (BY
SQ SEQUENCE 145 AA, 16241 MW, 58363541A062E71 CRC64;
SIMILARITY)
Query Match 33.5%; Score 60; DB 1; Length 145;
Best Local Similarity 38.9%; Pred. No. 0.16;
Matches 14; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 3 LSLDVPGLRLLEQARYKARNQATNAQILAHV 38
Db 108 ISIDLTFHLRNMTEMARBNENCREQAGLNRYLDEV 143

RESULT 11
URL_CYPCA STANDARD; PRT; 145 AA.
AC P01146;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Urotensin I precursor.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
NCBI_Taxid=962;
RX SEQUENCE FROM N.A.
RX MEDLINE=86094380; PubMed=3484550;
RA Ichikawa T., Ichikawa T., Deguchi T.;
RT "Cloning and sequence analysis of cDNA encoding urotensin I
RT precursor."
RT Proc. Natl. Acad. Sci. U.S.A. 83:308-312(1986).
RL [2]
RX SEQUENCE OF 103-143.
RX MEDLINE=83090718; PubMed=6757895;
RA Ichikawa T., McMaster D., Lederis K., Kobayashi H.;
RT "Isolation and amino acid sequence of urotensin I, a vasoactive and
RT ACTH-releasing neuropeptide, from the carp (Cyprinus carpio)
RT urophysin."
RT Peptides 3:859-867(1982).
RL [3]
RX SEQUENCE OF 103-143, AND SYNTHESIS OF 103-143.
RX MEDLINE=84025881; PubMed=6313156;
RA Lederis K., Letter A., McMaster D., Ichikawa T., McCannell K.L.,
RA Rivier J., Rivier C., Vale W., Fryer J., Kobayashi Y.;
RT "Isolation, analysis of structure, synthesis, and biological actions
RT of urotensin I neuropeptides."
Can. J. Biochem. Cell Biol. 61:602-614(1983).
RL -1- FUNCTION: Urotensin is found in the teleost caudal neurosecretory
CC system. It has a suggested role in osmoregulation and as a
CC corticotropin-releasing factor. The nonhomologal portion of this
CC precursor may be a urotensin binding protein, urophysin.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC factor/urotensin I family.
CC -----
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DR EMBL; M11671; AAA49214.1; -.
DR PIR; A94096; LOCAL.
DR InterPro; IPR000187; corticoliberin.
DR InterPro; IPR003620; Urocortin_CRF.
DR Pfam; PF00473; CRF; 1.
DR PRINTS; PRO1612; CRPFAMILY.
DR PRODOM; PD005970; Urocortin_CRF; 1.
DR SMART; SM00039; CRF; 1.
DR PROSITE; PS00511; CRF; 1.
DR Hormone; Cleavage on pair of basic residues; Amidation; Signal.
KW SIGNAL
FT CHAIN 1 22
FT PEPTIDE 103 143 UROPHYSIN I. (POTENTIAL).
FT MOD_RES 143 143 AMIDATION (G-144 PROVIDE AMIDE GROUP).
SQ SEQUENCE 145 AA, 16249 MW, 4F16166A580E20FB CRC64;
Query Match 33.5%; Score 60; DB 1; Length 145;
Best Local Similarity 38.9%; Pred. No. 0.16;
Matches 14; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 3 LSLDVPGLRLLEQARYKARNQATNAQILAHV 38
Db 108 ISIDLTFHLRNMTEMARBNENCREQAGLNRYLDEV 143

RESULT 12
URL_ONCMY STANDARD; PRT; 165 AA.
AC O93448;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Urotensin I precursor.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Proteocephalopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_Taxid=8022;
RX SEQUENCE FROM N.A.
RX TISSUE=Hypothalamus;
RX MEDLINE=99346219; PubMed=10417230;
RA Barsyte D., Tipping D.R., Smart D., Conlon J.M., Baker B.I.,
RA Lovejoy D.A.;
RT "Rainbow trout (Oncorhynchus mykiss) urotensin-I: structural
RT differences between urotensin-I and urocortins."
RL Gen. Comp. Endocrinol. 115:169-177(1999).
RL -1- FUNCTION: Urotensin is found in the teleost caudal neurosecretory
CC system. It has a suggested role in osmoregulation and as a
CC corticotropin-releasing factor. The nonhomologal portion of this
CC precursor may be a urotensin binding protein, urophysin.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC factor/urotensin I family.
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CC -----
DR EMBL; AJ005264; CAA06461.1;
DR InterPro; IPR000187; corticoliberin.
DR InterPro; IPR003620; Urocortin_CRF.
DR Pfam; PF00473; CRF; 1.
DR PRINTS; PRO1612; CRPFAMILY.
DR PRODOM; PD005970; Urocortin_CRF; 1.
DR SMART; SM00039; CRF; 1.
DR PROSITE; PS00511; CRF; 1.
DR Hormone; Cleavage on pair of basic residues; Amidation; Signal.
KW SIGNAL
FT SIGNAL 1
FT 18
FT POTENTIAL.

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FT CHAIN 19 120 UROPHYSIN (POTENTIAL).
 FT PEPTIDE 123 163 UROTENSIN-1.
 FT MOD_RES 163 163 AMIDATION (G-164 PROVIDE AMIDE GROUP) (BY
 FT SIMILARITY).
 SQ SEQUENCE 165 AA; 18631 MW; 3263357EB7E33A1A CRC64;

Query March 33.5%; Score 60; DB 1; Length 165;
 Best Local Similarity 36.1%; Pred. NO. 0.18; Mismatches 14; Indels 0; Gaps 0;
 Matches 13; Conservative 9;

Qy 3 LSLDVPILGILRLLEQARYKARNOQATNAQILAHV 38
 Db 128 ISIDLTFLLRLNMLEMARIESQKEQAEINRKYLDEV 163

RESULT 13

CRF_XENIA STANDARD; PRT; 162 AA.

AC P49188;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Corticotropin precursor (Corticotropin-releasing factor) (CRF)
 DE Corticotropin releasing hormone).
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 CC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A. PubMed=1448118;
 RX MEDLINE=93078805; PubMed=1448118;
 RA Stenzel-Poore M.P., Helwein K.A., Stenzel P., Lee S., Vale W.W.;
 RT "Characterization of the genomic corticotropin-releasing factor (CRF)
 RT gene from Xenopus laevis: two members of the CRF family exist in
 RT amphibians.";
 RL Mol. Endocrinol. 6:1716-1724(1992).
 CC -1- FUNCTION: This hormone from hypothalamus regulates the release of
 CC corticotropin from pituitary gland (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
 CC factor/urotensin I family.
 CC
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 CC
 CC EMBL; S50096; A45324277.1; -.
 DR PIR; A45362; A45362.
 DR InterPro; IPR000187; corticotliberin.
 DR InterPro; IPR003620; urocortin_CRF.
 DR Pfam; PF00473; CRF; 1.
 DR PRINTS; PRO1612; CRFAMILY.
 DR ProDom; PD005970; Urocortin_CRF; 1.
 DR SMART; SM00039; CRF; 1.
 DR PROSITE; PS00511; CRF; 1.
 KW Hormone; Amidation; Hypothalamus; Cleavage on pair of basic residues;
 KW Signal.
 FT SIGNAL 1 24
 FT PROPEP 25 119
 FT PEPTIDE 120 160
 FT MOD_RES 160 160
 SQ SEQUENCE 162 AA; 17880 MW; 02E6906AC0A656CB CRC64;

Query Match 31.8%; Score 57; DB 1; Length 162;
 Best Local Similarity 39.4%; Pred. No. 0.48;
 Matches 13; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 3 LSLDVPILGILRLLEQARYKARNOQATNAQIL 35

Db 125 ISIDLTFLLRLNMLEMARIESQKEQAEINRKYLDEV 157

RESULT 14

CRF_RAT STANDARD; PRT; 187 AA.

AC P01143;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Corticotropin precursor (Corticotropin-releasing factor) (CRF)
 DE Corticotropin releasing hormone).
 GN CRH.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. PubMed=3876950;
 RX MEDLINE=86030658; PubMed=3876950;
 RA Jingami H., Mizuno N., Takahashi H., Shibahara S., Furutani Y.,
 RA Imura H., Numa S.;
 RT "Cloning and sequence analysis of cDNA for rat
 RT corticotropin-releasing factor precursor.";
 RL FEBS Lett. 191:63-66(1985).
 RN [2]
 RP SEQUENCE FROM N.A. TISSUE=Liver;
 RC MEDLINE=90331928; PubMed=3274895;
 RX MEDLINE=90331928; PubMed=3274895;
 RA Thompson R.C., Seasholtz A.F., Herbert E.;
 RT "Rat corticotropin-releasing hormone gene: sequence and
 RT tissue-specific expression.";
 RL Mol. Endocrinol. 1:363-370(1987).
 RN [3]
 RP SEQUENCE OF 145-195.
 RX MEDLINE=83273710; PubMed=6603620;
 RA Rivier J., Spiess U., Vale W.;
 RT "Characterization of rat hypothalamic corticotropin-releasing
 RT factor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4851-4855(1983).
 CC -1- FUNCTION: This hormone from hypothalamus regulates the release of
 CC corticotropin from pituitary gland.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
 CC factor/urotensin I family.
 CC
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 CC
 CC EMBL; X03036; CAA26838.1; -.
 DR EMBL; M54987; AAA40965.1; -.
 DR PIR; A40906; RHRTCE.
 DR InterPro; IPR000187; corticotliberin.
 DR InterPro; IPR003620; Urocortin_CRF.
 DR Pfam; PF00473; CRF; 1.
 DR PRINTS; PRO1612; CRFAMILY.
 DR ProDom; PD005970; Urocortin_CRF; 1.
 DR SMART; SM00039; CRF; 1.
 DR PROSITE; PS00511; CRF; 1.
 KW Hormone; Amidation; Hypothalamus; Cleavage on pair of basic residues;
 KW Signal.
 FT SIGNAL 1 24
 FT PROPEP 25 144
 FT PEPTIDE 145 185
 FT MOD_RES 185 185
 SQ SEQUENCE 187 AA; 20680 MW; 911602C82A444FCB CRC64;

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OM protein - protein search, using sw model

Run on: April 20, 2004, 18:52:07 ; Search time 6.84 Seconds
(without alignments)
534.397 Million cell updates/sec

Title: US-09-919-473-11

Perfect score: 179
Sequence: 1 VILSLDVPILGIRILIEQARYKARNQATNAQIIAHV 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	34.1	41	1 UOCCIM	urotensin I - whit
2	60	33.5	122	2 S60262	corticotensin - ra
3	60	33.5	145	1 UOCC1	urotensin I precu
4	57	31.8	41	1 RHRGCE	corticoliberin - p
5	57	31.8	162	2 A43362	corticoliberin pre
6	57	31.8	187	1 RHRICE	corticoliberin pre
7	57	31.8	196	2 A30327	corticoliberin pre
8	56	31.3	162	2 A31343	corticoliberin 1 p
9	54	30.2	41	2 A43978	urotensin I - Euro
10	54	30.2	162	2 S14597	corticoliberin 2 p
11	53	29.6	40	1 SWRGS	sausage - Sauvag
12	52	29.1	393	2 T04957	hypothetical prote
13	51	28.5	412	2 F87709	DNA/paraoctanate m
14	50.5	28.2	1325	2 T01037	hypothetical prote
15	50	27.9	159	2 AB1557	methylated-DNA-pro
16	50	27.9	190	1 RSHSCE	corticoliberin pre
17	50	27.9	410	2 AG2693	large terminase [i
18	50	27.9	419	2 D97475	probable large ter
19	50	27.9	875	2 T43522	condensin complex
20	49.5	27.7	288	2 AB1608	phosphotransbutyry
21	49.5	27.7	639	2 T16648	hypothetical prote
22	49	27.4	214	2 AH0265	probable membrane
23	49	27.4	462	2 G83000	probable two-compo
24	49	27.4	750	2 C87159	cation-transportin
25	49	27.4	750	2 S77653	cation-transportin
26	48.5	27.1	238	2 AH0106	hypothetical prote
27	48.5	27.1	901	2 E70778	probable acee prot
28	48	26.8	239	2 C83637	probable ATP-bind
29	48	26.8	270	2 B75581	probable cytochrom

30	48	26.8	278	2 D83080	hypothetical prote
31	48	26.8	342	2 S23438	hypothetical prote
32	48	26.8	442	2 A71433	hypothetical prote
33	48	26.8	450	2 C75316	conserved hypotet
34	48	26.8	492	2 T26936	hypothetical prote
35	48	26.8	573	2 T10037	hypothetical prote
36	48	26.8	585	2 A84346	subtilisin homolog
37	48	26.8	772	2 T25469	hypothetical prote
38	48	26.8	833	1 A31593	heat shock transcr
39	48	26.8	919	2 T29581	hypothetical prote
40	48	26.8	1033	2 A96714	hypothetical prote
41	48	26.8	1122	2 T42400	Eph receptor tyros
42	47.5	26.5	105	1 RGECMJ	Met regulon regula
43	47.5	26.5	105	2 A23081	regulatory protein
44	47.5	26.5	105	2 C91237	repressor protein
45	47.5	26.5	105	2 G86084	repressor of all m

ALIGNMENTS

RESULT 1
UOCCIM
urotensin I - white sucker
C/Species: Calostomus commersoni (white sucker)
C/Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 21-Jan-2000
C/Accession: A94267; A90754; A01407
R/Identifier: K.; Letter, A.; McMaster, D.; Moore, G.; Schlesinger, D.
Science 218, 162-164, 1982
A/Title: Complete amino acid sequence of urotensin I, a hypotensive and corticotropin-rel
A/Reference number: A94267; MUID:8301606; PMID:6581844
A/Accession: A94267
A/Molecule type: protein
A/Residues: 1-41 <LR2>
R/Identifier: K.; Letter, A.; McMaster, D.; Ichikawa, T.; MacCannell, K.L.; Rivier, J.; Riv
Can J. Biochem. Cell Biol 61, 602-614, 1983
A/Title: Isolation, analysis of structure, synthesis, and biological actions of urotensin
A/Reference number: A90754; MUID:84025861; PMID:6513156
A/Accession: A90754
A/Molecule type: protein
A/Residues: 1-41 <LR2>
C/Comment: Urotensin I is found in the teleost caudal neurosecretory system and is invol
C/Superfamily: corticoliberin-endorphinliberin; diuretic hormone homology
C/Keywords: amidated carboxyl end; hormone; osmoregulation
F/1-41/Domain: diuretic hormone homology <DHR>
F/41/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 34.1%; Score 61; DB 1; Length 41;
Best Local Similarity 38.9%; Pred. No. 0.041;
Matches 14; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 3 LSLDVPILGIRILIEQARYKARNQATNAQIIAHV 38
DB 6 ISIDLPHLRIMNIEWARIENEREQGLNKYIDEV 41

RESULT 2
S60262
corticotensin - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jan-2003
C/Accession: S60262
R/Vaughan, J.; Donaldson, C.; Bittencourt, J.; Perrin, M.H.; Lewis, K.; Sutton, S.; Chan
Nature 378, 287-292, 1995
A/Title: Urocortin, a mammalian neuropeptide related to fish urotensin I and to corticot
A/Reference number: S60262; MUID:96065765; PMID:7477349
A/Accession: S60262
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-122 <VAU>
A/Cross-references: EMBL:U33935; NID:q1065908; PIR:AA87566.1; PID:q1065909
C/Superfamily: corticoliberin-endorphinliberin; diuretic hormone homology
F/80-120/Domain: diuretic hormone homology <DHR>

```

Query Match 33.5% Score 60; DB 2; Length 122;
Best Local Similarity 44.4% Pred. No. 0.2;
Matches 16; Conservative 5; Mismatches 15; Indels 0; Gaps 0;
QY 3 LSLDVPIGLRITLLEQARYKAARQNAQAQILAHV 38
      |||:|||||:|:|:|
Db 85 LSLDIFHLIKRTLLRLAKAQQREARAGRIIPSV 120

```

RESULT 3
VOCAL

C:Species: *Cyprinus carpio* (common carp)
C:Date: 05-Apr-1993 #sequence revision 31-Mar-1998 #text_change 20-Apr-2001
C:Accession: A94096; A93552; X01408; A25966
R:1tsnida, I.; Ichikawa, T.; Deguchi, T.
Proc. Natl. Acad. Sci. U.S.A. 83, 308-312, 1986
A:Title: Cloning and sequence analysis of cDNA encoding uterensin I precursor.
A:Reference number: A94096; MUID:86094380; PMID:3484550
A:Accession: A94096
A:Molecule type: mRNA
A:Residues: 1-145 <ISH>
A:Cross-references: GB:M1671; NID:g213064; PIND:AAA49214.1; PID:g213065
A:Experimental source: Spinal cord
R:Ichikawa, T.; McMaster, D.; Lederis, K.; Kobayashi, H.
Peptides 3, 859-867, 1982
A:Title: Isolation and amino acid sequence of uterensin I, a vasoactive and ACTH-releasing peptide.
A:Reference number: A93752; MUID:83090718; PMID:657895
A:Accession: A93752
A:Molecule type: protein
A:Residues: 105-143 <ICH>
C:Comment: Uterensin I is found in the teleost caudal neurosecretory system. It has a unique structure with a disulfide bridge between the Cys105 and Cys143 residues.
C:Comment: The nonhormonal portion of this precursor may be a uterensin binding protein.
C:Superfamily: corticosteroid-binding globulin; diuretic hormone homologous
C:Keywords: amidated carboxyl end; hormone; osmoregulation
E:1-32/Domain: signal sequence #status predicted <SIG>
E:23-14/Domain: signal sequence #status predicted <SIG>
E:103-143/Product: uterensin I #status predicted <MAT>
E:103-143/Domain: diuretic hormone homologous <DHR>
E:143/Modified site: amidated carboxyl end (Val) (amide in mature form from following glycosylation)

Query Match 33.5%; Score 60; DB 1; Length 145;

```
Matches 14; Conservative 7; Mismatches 15; Indels 0; Gaps 0
```

```

QY      3  LSLDVPGLRILLLEQARKKAPRNQATNQAIIAHV 38
      : : : : : : : : : : : : : : : : : :
Db     108 ISIDLTFHLIRNMIEARNENQREGAGINRKYLDEV 14

```

RESULT 4

corticotiberin - pig
 N/Alternate names: corticotropin-releasing factor; CRF; endorphiniberin
 C/Species: Sus scrofa domestica (domestic pig)
 C/date: 30-Jun-1987 #sequence_revision 30-Jun-1997 #text_change 11-Apr-1997
 C/accession: A01404
 R/Pathy, M.; Horvath, U.; Mason-Garcia, M.; Szoke, B.; Schlessinger, D.H.; Schally, A.V.
 Proc. Natl. Acad. Sci. U.S.A. 82, 8762-8766, 1985
 A/Title: Isolation and amino acid sequence of corticotropin-releasing factor from pig hypothalamus
 A/Reference number: A01404; MUID:86094305; PMID:3878520
 A/Accession: A01404

Molecule type: protein

;Note: 40-11e was also found

Superfamily: corticotiberin-endorpholiberin; diuretic hormone homology

F;41/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 31.8%; Score 57; DB 1; Length 41;

Best Local Similarity 39.4%; Pred. No. 0.16;
Matches 13; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

```

QY      3 ISLDVPIGLRILLGEARFYKARNQATNAQL 35
        :|||: |||: |||: |||: |||: |||:
Db      6 ISLDITPHLRVFLMARAEQLAQQAHSNRKM 38

```

RESULT 5

corticotiberinprecursor - African clawed frog
 N:Alternate names: corticotropin-releasing factor
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 17-Feb-1994 #revision 17-Feb-1994 #next_change 16-Jul-1999
 C:Accession: A45362
 R:Stenzel-Poore, M.P.; Heldwein, K.A.; Stenzel, P.; Lee, S.; Vale, W.W.
 Mol. Endocrinol. 6, 1718-1724, 1992
 A:Title: Characterisation of the genomic corticotropin-releasing factor (CRF) gene from *Xenopus laevis*
 A:Reference number: A45362; PMID:93078805; PMID:1448118
 A:Accession: A45362
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-162 <SP>
 A:Cross-references: GB:850096; NID:5260494; PIDN:PAAB24277.1; PID:5260495
 A:Note: sequence extracted from NCBI backbone (NCBI:P.118818)
 C:Genetic: CRF
 A:Gene: CRF
 C:Superfamily: corticotiberin-endorpholiberin; diuretic hormone homology
 C:Keywords: amidated carboxyl end; hormone; hypothalamus
 C:120-160/Domain: diuretic hormone homology <DB>

Query Match	Score	DB	Length
31.8%	57	2	162

Matches 13; Conservative 8; Mismatches 12; Indels 0; Gaps 0.

```
QY      3 LSLDVPIGLIRILLEQRARYKARNQATNAQTIL    35
       :|||:|||:|||||:|||||:|||||:|||||:
Db     125 ISLDLTFTHLRLEVLEMARAEQIAQAHSNRKLIM   15
```

RESULT
PHRTCE

Alternate names: corticotropin-releasing factor; prepro-CRF

```

;Species: Rattus norvegicus (Norway rat)
Date: 14-Nov-1993 #Procurement revision 30-Sep-1997 #text change 18-Jun-1999

```

C. Thompson: A40906; A91351; A93965; A01405; A24009
R. Thompson, R.C.; Seasholtz, A.F.; Herbert, E.
Mol. Endocrinol. 1, 363-370, 1987

A;Accession: A40906

A:Residues: 1-187 <GB>
A:Cross-references: GB:MS4987; NID:G203593; PIRN:AAA0965.1; PID:G203594
R:Utingami, H.; Mizuno, N.; Takahashi, H.; Shibahara, S.; Furutani, Y.; Imura, H.; Numa, S.
FEBS Lett. 191, 63-66, 1985
Article: Cloning and sequence analysis of cDNA for rat corticotropin-releasing factor precursor
A:Reference number: A91351; MUID:86030658; PMID:3876950
A:Accession: A91351
A:Molecule type: mRNA
A:Residues: 1-187 <JN>
A:Cross-references: GB:JX03036; NID:G56008; PIDN:CAA2638.1; PID:G56009

Rivier, J.; Spiess,

A; Title: Characterization of rat h

A/Accession: A93965

A; Residues: 145-185 <RIV>

tary gland, testis, spinal cord, and adrenal gland.

C/Genetics:
 A/Gene: CRH
 A/Introns: #status absent
 A/Note: one intron is in 5', noncoding region
 C/Superfamily: corticotropin-releasing factor
 C/Keywords: amidated carboxyl end; hormone; hypothalamus
 F/1-24/Domain: signal sequence #status predicted <SIG>
 F/125-187/Product: precorticotropin #status predicted <MAT>
 F/145-185/Product: corticotropin #status experimental <CLN>
 F/145-184/Domain: diuretic hormone homology <DHR>
 F/185/Modified site: amidated carboxyl end (ile) (amide in mature form from following gl)

Query Match 31.8%; Score 57; DB 1; Length 187;
 Best Local Similarity 39.4%; Pred. No. 0.88;
 Matches 13; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 3 LSLDVPGLRLILLEQARYKAARNOATNAQIL 35
 Db 150 ISLDLTFHLRLVLEWARRAQALQAHSNRKLM 182

RESULT 7

Corticotropin precursor - human
 N/Alternate names: corticotropin-releasing factor
 N/Contains: corticotropin
 C/Species: Homo sapiens (man)
 C/Date: 07-Sep-1990 #sequence revision 07-Sep-1990 #text_change 16-Jul-1999
 C/Accession: A30327; A60860; I38106
 R/Robinson, B.G.; D'Angio Jr, L.A.; Pasieka, K.B.; Majzoub, J.A.
 Mol. Cell. Endocrinol. 61, 175-180, 1989
 A/Title: Preprocorticotropin releasing hormone: cDNA sequence and in vitro processing.
 A/Reference number: A30327; MUID:89137721; PMID:2783917
 A/Accession: A30327
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA

A/Residues: 1-196 <ROB>
 R/Sasaki, A.; Tempst, P.; Liotta, A.S.; Margioris, A.N.; Hood, L.E.; Kent, S.B.H.; Sato, J.
 Clin. Endocrinol. Metab. 67, 768-773, 1988
 A/Title: Isolation and characterization of a corticotropin-releasing hormone-like peptide
 A/Reference number: A60860; MUID:8831316; PMID:3262120
 A/Accession: A60860
 A/Molecule type: protein

A/Residues: 154-168, 'X', 170-186 <SAS>
 R/Shibahara, S.; Morimoto, Y.; Furutani, Y.; Notake, M.; Takahashi, H.; Shimizu, S.; Horikawa, U.
 J. Biol. Chem. 268, 775-779, 1993
 A/Title: Isolation and sequence analysis of the human corticotropin-releasing factor precursor
 A/Reference number: I38106; MUID:84057755; PMID:6605851
 A/Accession: I38106
 A/Status: preliminary; translated from GB/EMBL/DBJ

A/Residues: 1-196 <RES>
 A/Cross-references: EMBL:V00571; NID:G35355; PIND:CAA23834.1; PID:G35356
 C/Genetics:
 A/Gene: GDB:CRH

A/Cross-references: GDB:119804; OMIM:122560
 A/Map position: 8q13-8q13
 C/Superfamily: corticotropin-endorphin; diuretic hormone homology
 C/Keywords: amidated carboxyl end; hormone; hypothalamus; placenta
 F/1-24/Domain: signal sequence #status predicted <SIG>
 F/125-187/Product: precorticotropin #status predicted <MAT>
 F/145-185/Product: corticotropin #status predicted <CLN>
 F/145-184/Domain: diuretic hormone homology <DHR>
 F/185/Modified site: amidated carboxyl end (ile) (amide in mature form from following gl)

Query Match 31.8%; Score 57; DB 2; Length 196;
 Best Local Similarity 39.4%; Pred. No. 0.93;
 Matches 13; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 3 LSLDVPGLRLILLEQARYKAARNOATNAQIL 35
 Db 159 ISLDLTFHLRLVLEWARRAQALQAHSNRKLM 191

RESULT 8
 A31343
 Corticotropin 1 precursor - white sucker
 N/Contains: corticotropin 1
 C/Species: Catostomus commersoni (white sucker)
 C/Date: 31-Mar-1990 #sequence revision 31-Mar-1990 #text_change 16-Jul-1999
 C/Accession: A31343
 R/Okawara, Y.; Morley, S.D.; Burzio, L.O.; Zwiers, H.; Lederis, K.; Richter, D.
 Proc. Natl. Acad. Sci. U.S.A. 85, 8439-8443, 1988
 A/Title: Cloning and sequence analysis of cDNA for corticotropin-releasing factor precursor
 A/Reference number: A31343; MUID:89042139; PMID:3186733
 A/Accession: A31343
 A/Molecule type: mRNA
 A/Residues: 1-162 <OKA>
 C/Superfamily: corticotropin-endorphin; diuretic hormone homology
 C/Keywords: amidated carboxyl end; hormone
 F/1-24/Domain: (or 1-27 or 1-28 or 1-29) signal sequence #status predicted <SIG>
 F/125-162/Product: (or 28-162 or 29-162 or 30-162) precorticotropin #status predicted <MAT>
 F/120-159/Product: corticotropin 1 #status predicted <CLN>
 F/120-159/Domain: diuretic hormone homology <DHR>
 F/160/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gl)

Query Match 31.3%; Score 56; DB 2; Length 162;
 Best Local Similarity 39.4%; Pred. No. 1.1;
 Matches 13; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 3 LSLDVPGLRLILLEQARYKAARNOATNAQIL 35
 Db 125 ISLDLTFHLRLVLEWARRAQALQAHSNRKLM 157

RESULT 9

A43978
 Urotensin I - European flounder
 C/Species: Platichtys fleuss (European flounder)
 C/Date: 11-Feb-1993 #sequence revision 11-Feb-1993 #text_change 17-May-1996
 C/Accession: A43978
 R/Conlon, J.M.; Arnold-Reed, D.E.; Belmont, R.J.
 Peptides 11, 891-895, 1990

A/Title: Urotensin I and its N-terminal flanking peptide from the flounder, Platichtys
 A/Reference number: A43978
 A/Accession: A43978
 A/Status: preliminary
 A/Molecule type: protein

A/Residues: 1-41 <CON>
 C/Superfamily: corticotropin-endorphin; diuretic hormone homology
 F/1-41/Domain: diuretic hormone homology <DHR>

Query Match 30.2%; Score 54; DB 2; Length 41;
 Best Local Similarity 30.6%; Pred. No. 0.44;
 Matches 11; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

Qy 3 LSLDVPGLRLILLEQARYKAARNOATNAQIL 38
 Db 6 MSIDLTFHLRLVLEWARRAQALQAHSNRKLM 41

RESULT 10

S14597
 Corticotropin 2 precursor - white sucker
 N/Alternate names: corticotropin-releasing factor 2
 N/Contains: corticotropin 2
 C/Species: Catostomus commersoni (white sucker)

C/Date: 21-Nov-1993 #sequence revision 18-Nov-1994 #text_change 22-Oct-1999
 C/Accession: S14597
 R/Morley, S.D.; Schoenrock, C.; Okawara, Y.; Lederis, K.; Richter, D.
 submitted to the EMBL Data Library, March 1991
 A/Description: Corticotropin-releasing factor (CRF) gene family in the brain of the teleost
 one urotensin I peptide.
 A/Reference number: S14597
 A/Accession: S14597

A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-162 <MOR>
 A:Cross-references: EMBL:X58784; NID:g62599; PIDD:CA4159.1; PID:g62600
 C:Superfamily: corticoliberin-endorpholiberin; diuretic hormone homology
 C:Keywords: amidated carboxyl end; hormone
 F:1-24/Domin: (or 1-27 or 1-28 or 1-29) signal sequence #status predicted <SIG>
 F:125-162/Product: (or 28-162 or 29-162 or 30-162) procorticoliberin #status predicted <M>
 F:120-160/Product: corticoliberin 2 #status predicted <CLN>
 F:120-159/Domin: diuretic hormone homology <DMH>
 F:160/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gl

Query Match 30.2%; Score 54; DB 2; Length 162;
 Best Local Similarity 39.4%; Pred. No. 2.1;
 Matches 13; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 3 LSLDVPGLRLLEQARYKARNOAATNQIL 35
 DB 125 ISLDLTHLREVLKMAEQALVQAHSNRKM 157

RESULT 11

SMFGS
 Sauvagine - Sauvage's leaf frog
 C:Species: Phyllomedusa sauvagei (Sauvage's leaf frog)
 C>Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 07-May-1999
 C:Accession: A01406; A61325
 R:Montecuchi, P.C.; Henschen, A.; Erepaner, V.
 R:Montecuchi, P.C.; Henschen, A.; Erepaner, V.
 Hope-Sevler's Z. Physiol. Chem. 360, 1178, 1979
 A>Title: Structure of sauvagine, a vasoactive peptide from the skin of a frog.
 A:Reference number: A01406

A:Molecule type: protein
 A:Residues: 1-40 <MON>
 R:Montecuchi, P.C.; Henschen, A.
 Int. J. Pept. Protein Res. 18, 113-120, 1981
 A>Title: Amino acid composition and sequence analysis of sauvagine, a new active peptide
 A:Reference number: A61325; MUID:82075075; PMID:7309372
 A:Accession: A61325
 A:Molecule type: protein
 A:Residues: 1-40 <MO2>
 C:Comment: This hypotensive peptide is obtained from the cutaneous tissue of the frog.
 C:Superfamily: corticoliberin-endorpholiberin; diuretic hormone homology
 C:Keywords: amidated carboxyl end; antihypertensive; pyroglutamic acid; skin
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:40/Modified site: amidated carboxyl end (Ile) #status experimental

Query Match 29.6%; Score 53; DB 1; Length 40;
 Best Local Similarity 33.3%; Pred. No. 0.6;
 Matches 11; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 3 LSLDVPGLRLLEQARYKARNOAATNQIL 35
 DB 5 ISLDLTHLREVLKMAEQALVQAHSNRKM 157

RESULT 12

T04957
 hypothetical protein F7J7.200 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
 C:Accession: T04957
 R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X
 submitted to the Protein Sequence Database, July 1998
 A:Reference number: Z15391
 A:Accession: T04957
 A:Molecule type: DNA
 A:Residues: 1-393 <BEV>
 A:Cross-references: EMBL:AL021960
 A:Experimental source: cultivar Columbia; BAC clone F7J7
 C:Genetics:
 A:Map position: 4
 A:introns: 80/1; 217/3; 264/1; 291/3

A>Note: F7J7.200

Query Match 29.1%; Score 52; DB 2; Length 393;
 Best Local Similarity 27.3%; Pred. No. 11;
 Matches 9; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

QY 1 VLSLDVPGLRLLEQARYKARNOAATNQI 33
 DB 231 ILSLQIRLALVFTILASRRESIQESISNGE 263

RESULT 13

F87709
 DNA/pantothenate metabolism flavoprotein [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
 C:Accession: F87709
 R:Nierman, W.C.; Feldlyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.I.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gilm, M.L.; Hatt, D.H.; Kolme
 n, J.; Esmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A>Title: Complete genome sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173696; PMID:11259647
 A:Accession: F87709
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-412 <STO>
 A:Cross-references: GB:AE005673; NID:g13425480; PIDD:AAK25674.1; GSPDB:GN00148
 C:Genetics:
 A:Gene: CC3712
 C:Superfamily: pantothenate metabolism flavoprotein dfr

Query Match 28.5%; Score 51; DB 2; Length 412;
 Best Local Similarity 40.6%; Pred. No. 16;
 Matches 13; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 3 LSLDVPGLRLLEQARYKARNOAATNQI 34
 DB 252 VALPTPEGRIDVETAKQMLAASQALPADV 283

RESULT 14

T01037
 hypothetical protein YUP8H12R.20 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 22-Oct-1999
 C:Accession: T01037
 R:Thellogis, A.; Vysotskaja, V.S.; Osborne, B.I.; Schwartz, J.R.; Federspiel, N.A.; Kwan,
 Oefner, P.; Davis, R.W.
 submitted to the EMBL Data Library, May 1998
 A:Description: Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence.
 A:Reference number: Z14227
 A:Accession: T01037
 A:Molecule type: DNA
 A:Residues: 1-1325 <THE>
 A:Cross-references: EMBL:AC002986; NID:g2494106; PID:g3152582; GSPDB:GN00059; ATSP:YUP8H1
 C:Genetics:
 A:Gene: ATSP:YUP8H12R.20
 A:Map position: 1
 A:introns: 70/4; 130/3; 233/3; 384/3; 450/3; 470/1; 687/3; 740/3; 765/3; 868/3; 940/3; 11

Query Match 28.2%; Score 50.5; DB 2; Length 1325;
 Best Local Similarity 31.2%; Pred. No. 71;
 Matches 15; Conservative 5; Mismatches 11; Indels 17; Gaps 1;

QY 5 LSLDVPGLRLLEQARYKARNOAATNQI 35
 DB 461 LDIPLGFRKLVSEVRKVEINGEDWQSCNRTGSGQLVROAATACTL 528

RESULT 15

AB1557

methylated-DNA-protein-cysteine methyltransferase homolog lin0995 [imported] - *Listeria*
 C/Species: *Listeria innocua*
 C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 11-Jan-2002
 C/Accession: AB1557
 R/Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
 .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; Fsihi, H.
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.; Ma
 ck, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
 A./Title: Comparative genomics of *Listeria* species.
 A/Reference number: AB1077; MUID:21537279; PMID:11679669
 A/Accession: AB1557
 A/Status: Preliminary
 A/Molecule type: DNA
 A/Residues: 1-159 <GLA>
 A/Cross-references: GB:AL592022; PIDN:CAC96226.1; PID:G16413454; GSPDB:GN00178
 A/Experimental source: strain Clp11262
 C/Genetics:
 A/Gene: lin0995
 C/Superfamily: methylated-DNA-protein-cysteine S-methyltransferase; methylated-DNA-prote
 C/Keywords: methylated amino acid
 F/125/Binding site: methyl (Cys) (covalent) #status predicted

Query Match 27.9%; Score 50; DB 2; Length 159;
 Best Local Similarity 38.7%; Pred. No. 7.8; Mismatches 0; Gaps 0;
 Matches 12; Conservative 4; Indels 15;

QY 6 DVPIGLRILLEQARYKAAQNQAATNAQILA 36
 DB 7 DSPVGTLPILIEDAHITKISYDEPTNWEILA 37

Search completed: April 20, 2004, 18:57:23
 Job time : 7.84 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 20, 2004, 18:56:48 ; Search time 57.4933 Seconds

(without alignments)
537.026 Million cell updates/sec

Title: US-09-919-473-10

Perfect score: 557
Sequence: 1 MTRNALVVFVLMMDRIIFV.....KAANOATNAQILAHVGR 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1124875 seqs, 275673149 residues

Total number of hits satisfying chosen parameters: 1124875

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/1/pubpa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpa/US07_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpa/US08_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/1/pubpa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpa/US10_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/1/pubpa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	557	100.0	112	9	US-09-919-473-10
2	312	56.0	112	9	US-09-682-706-2
3	312	56.0	112	9	US-09-919-473-2
4	179	32.1	38	9	US-09-919-473-11
5	179	32.1	38	10	US-09-799-978-43
6	179	32.1	38	14	US-10-099-766-9
7	145	26.0	41	9	US-09-919-473-3
8	140	25.1	38	14	US-10-315-964A-114
9	140	25.1	38	14	US-10-317-251A-114
10	139	25.0	38	14	US-10-317-252A-114
11	139	25.0	38	9	US-09-919-473-4
12	139	25.0	38	10	US-09-799-978-44
13	139	25.0	38	14	US-10-099-766-8
14	139	25.0	38	14	US-10-315-964A-4
15	139	25.0	38	14	US-10-315-964A-123

16	139	25.0	38	14	US-10-315-964A-354	Sequence 354, App
17	139	25.0	38	14	US-10-317-251A-4	Sequence 4, Appl1
18	139	25.0	38	14	US-10-317-251A-123	Sequence 123, App
19	139	25.0	38	14	US-10-317-251A-354	Sequence 354, App
20	139	25.0	38	14	US-10-317-252A-4	Sequence 4, Appl1
21	139	25.0	38	14	US-10-317-252A-123	Sequence 123, App
22	139	25.0	38	14	US-10-317-252A-354	Sequence 354, App
23	139	25.0	39	14	US-10-315-964A-356	Sequence 356, App
24	139	25.0	39	14	US-10-315-964A-368	Sequence 368, App
25	139	25.0	39	14	US-10-317-251A-356	Sequence 356, App
26	139	25.0	39	14	US-10-317-251A-368	Sequence 368, App
27	139	25.0	39	14	US-10-317-252A-356	Sequence 356, App
28	139	25.0	39	14	US-10-317-252A-368	Sequence 368, App
29	138	24.8	38	14	US-10-315-964A-122	Sequence 122, App
30	138	24.8	38	14	US-10-317-251A-122	Sequence 122, App
31	138	24.8	38	14	US-10-317-252A-122	Sequence 122, App
32	137	24.6	38	14	US-10-315-964A-110	Sequence 110, App
33	137	24.6	38	14	US-10-317-251A-110	Sequence 110, App
34	137	24.6	38	14	US-10-317-252A-110	Sequence 110, App
35	136	24.4	38	14	US-10-315-964A-109	Sequence 109, App
36	136	24.4	38	14	US-10-315-964A-124	Sequence 124, App
37	136	24.4	38	14	US-10-315-964A-127	Sequence 127, App
38	136	24.4	38	14	US-10-315-964A-130	Sequence 130, App
39	136	24.4	38	14	US-10-317-251A-109	Sequence 109, App
40	136	24.4	38	14	US-10-317-251A-124	Sequence 124, App
41	136	24.4	38	14	US-10-317-251A-127	Sequence 127, App
42	136	24.4	38	14	US-10-317-252A-109	Sequence 109, App
43	136	24.4	38	14	US-10-317-252A-124	Sequence 124, App
44	136	24.4	38	14	US-10-317-252A-127	Sequence 127, App
45	136	24.4	38	14	US-10-317-252A-127	Sequence 127, App

ALIGNMENTS

RESULT 1
US-09-919-473-10
Sequence 10, Application US/09919473
Patent No. US20020127221A1
GENERAL INFORMATION:
APPLICANT: Vale, Wylie Walker Jr.
APPLICANT: Lewis, Kathy Ann
APPLICANT: Reyes, Teresa Marie
APPLICANT: Hogenesch, John Beren
APPLICANT: Sawchenko, Paul Emil
APPLICANT: Vaughan, Joan Maureen
APPLICANT: Rivier, Jean Edouard Frederic
TITLE OR INVENTION: Urocortin Proteins and Uses Thereof
FILE REFERENCE: D6334
CURRENT APPLICATION NUMBER: US/09/919,473
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/273,569
PRIOR FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 10
LENGTH: 112
TYPE: PRT
ORGANISM: Mus musculus
FEATURES:
OTHER INFORMATION: Mouse Urocortin II precursor peptide
US-09-919-473-10
Query Match 100.0%; Score 557; DB 9; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.4e-52;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MTRNALVVFVLMMDRIIFVPGTPIPTFQILPONSLETTSSVTSSESSSGTTGPAASNS 60
1 MTRNALVVFVLMMDRIIFVPGTPIPTFQILPONSLETTSSVTSSESSSGTTGPAASNS 60
61 NSKASPLDTRVLISDVPDGLRIILEQARYAANOATNAQILAHVGR 112

Db 61 NSKASPYLDRVILSLDVPILGLILBQARYKARNOATNAQILAHV 112

RESULT 2

US-09-682-706-2

Sequence 2, Application US/09682706

Patent No. US20020082409A1

GENERAL INFORMATION:

APPLICANT: Hsu, Sheau-Yu

APPLICANT: Heuhen, Aaron

TITLE OF INVENTION: Stresscoping and their ses

FILE REFERENCE: STAN210

CURRENT APPLICATION NUMBER: US/09/682,706

CURRENT FILING DATE: 2001-10-09

PRIOR APPLICATION NUMBER: 60/276,615

PRIOR FILING DATE: 2001-03-15

PRIOR APPLICATION NUMBER: 60/244,128

PRIOR FILING DATE: 2000-10-26

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 112

TYPE: PRT

ORGANISM: Homo Sapiens

US-09-682-706-2

Query Match

Best Local Similarity 56.0%; Score 312; DB 9; Length 112;

Matches 67; Conservative 15; Mismatches 28; Indels 0; Gaps 0;

QY 1 MTRMALVVFVVLMLDRILFVPGTPIPTFQLLPQNSLETPSSVTSSSGTTGPASWS 60

Db 1 MTRCALLMLVLMGLRVLVVPTPIPTFQLLPQNSQTPRPAASPSAPPTWPAAS 60

QY 61 NSKASPYLDRVILSLDVPILGLILBQARYKARNOATNAQILAHV 110

Db 61 HCSPTRHPSRIVSLDVPILGLILBQARAPARAEQATNARILARVG 110

RESULT 3

US-09-919-473-2

Sequence 2, Application US/09919473

Patent No. US20020127221A1

GENERAL INFORMATION:

APPLICANT: Vale, Wylie Walker Jr.

APPLICANT: Lewis, Kathy Ann

APPLICANT: Reyes, Teresa Marie

APPLICANT: Hogenesch, John Beren

APPLICANT: Sawchenko, Paul Emil

APPLICANT: Vaughan, Joan Maureen

APPLICANT: Rivier, Jean Edouard Frederic

APPLICANT: Perrin, Marilyn Heller

TITLE OF INVENTION: Urocortin Proteins and Uses Thereof

FILE REFERENCE: D6334

CURRENT APPLICATION NUMBER: US/09/919,473

CURRENT FILING DATE: 2001-07-31

PRIOR APPLICATION NUMBER: US 60/273,969

PRIOR FILING DATE: 2001-03-07

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 2

LENGTH: 112

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Human Urocortin-related peptide (hURP)

US-09-919-473-2

Query Match

Best Local Similarity 56.0%; Score 312; DB 9; Length 112;

Matches 67; Conservative 15; Mismatches 28; Indels 0; Gaps 0;

QY 1 MTRMALVVFVVLMLDRILFVPGTPIPTFQLLPQNSLETPSSVTSSSGTTGPASWS 60

Db 61 NSKASPYLDRVILSLDVPILGLILBQARYKARNOATNAQILAHV 110

QY 61 HCSPTRHPSRIVSLDVPILGLILBQARAPARAEQATNARILARVG 110

RESULT 4

US-09-919-473-11

Sequence 11, Application US/09919473

Patent No. US20020127221A1

GENERAL INFORMATION:

APPLICANT: Vale, Wylie Walker Jr.

APPLICANT: Lewis, Kathy Ann

APPLICANT: Reyes, Teresa Marie

APPLICANT: Hogenesch, John Beren

APPLICANT: Sawchenko, Paul Emil

APPLICANT: Vaughan, Joan Maureen

APPLICANT: Rivier, Jean Edouard Frederic

APPLICANT: Perrin, Marilyn Heller

TITLE OF INVENTION: Urocortin Proteins and Uses Thereof

FILE REFERENCE: D6334

CURRENT APPLICATION NUMBER: US/09/919,473

CURRENT FILING DATE: 2001-07-31

PRIOR APPLICATION NUMBER: US 60/273,969

PRIOR FILING DATE: 2001-03-07

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 11

LENGTH: 38

TYPE: PRT

ORGANISM: Mus musculus

FEATURE:

OTHER INFORMATION: Mouse Urocortin II

US-09-919-473-11

Query Match

Best Local Similarity 32.1%; Score 179; DB 9; Length 38;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 VILSLDVPILGLILBQARYKARNOATNAQILAHV 109

Db 1 VILSLDVPILGLILBQARYKARNOATNAQILAHV 38

RESULT 5

US-09-799-978-43

Sequence 43, Application US/09799978

Publication No. US20030165807A1

GENERAL INFORMATION:

APPLICANT: The Procter & Gamble Company

APPLICANT: Isfort, Robert

APPLICANT: Sheldon, Russell

TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or

FILE REFERENCE: 8448

CURRENT APPLICATION NUMBER: US/09/799,978

CURRENT FILING DATE: 2001-03-06

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn version 3.0

SEQ ID NO 43

LENGTH: 38

TYPE: PRT

ORGANISM: Mus musculus

US-09-799-978-43

Query Match

Best Local Similarity 32.1%; Score 179; DB 10; Length 38;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 VILSLDVPILGLILBQARYKARNOATNAQILAHV 109

Db 1 VILSLDVPILGLILBQARYKARNOATNAQILAHV 38

RESULT 6
US-10-099-766-9
; Sequence 9, Application US/10099766
; Publication No. US20030036507A1
; GENERAL INFORMATION:
; APPLICANT: Lewis, Kathy
; APPLICANT: Vale, Wylie
; APPLICANT: Marilyn H. Perrin
; APPLICANT: Jean E. Rivier
; APPLICANT: Koichi S. Kunitake
; APPLICANT: Jozsef Guliyas
; TITLE OF INVENTION: Urocortin III and Uses Thereof
; FILE REFERENCE: D6390
; CURRENT APPLICATION NUMBER: US/10/099,766
; CURRENT FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/276,069
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 9
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: Mouse Urocortin II (mUcn II)
US-10-099-766-9

Query Match 32.1%; Score 179; DB 14; Length 38;
Best Local Similarity 100.0%; Pred. No. 4,8e-12;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 VIISLDVPIGLRIILBOARKYKARNOATNAQIIAHV 109
DB 1 IVISLDVPIGLRIILBOARKYKARNOATNAQIIAHV 38

RESULT 7
US-09-919-473-3
; Sequence 3, Application US/09919473
; Patent No. US2002012721A1
; GENERAL INFORMATION:
; APPLICANT: Vale, Wylie Walker Jr.
; APPLICANT: Lewis, Kathy Ann
; APPLICANT: Reyes, Teresa Marie
; APPLICANT: Hogenesche, John Beren
; APPLICANT: Sawchenko, Paul Emil
; APPLICANT: Vaughan, Joan Maureen
; APPLICANT: Rivier, Jean Edouard Frederic
; APPLICANT: Perrin, Marilyn Heller
; TITLE OF INVENTION: Urocortin Proteins and Uses Thereof
; FILE REFERENCE: D6334
; CURRENT APPLICATION NUMBER: US/09/919,473
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/273,969
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 3
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human Urocortin-related peptide (hURP)
US-09-919-473-3

Query Match 26.0%; Score 145; DB 9; Length 41;
Best Local Similarity 76.9%; Pred. No. 2,4e-08;
Matches 30; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 72 VIISLDVPIGLRIILBOARKYKARNOATNAQIIAHV 110
DB 1 IVISLDVPIGLRIILBOARKYKARNOATNAQIIAHV 39

RESULT 8
US-10-315-964A-114
; Sequence 114, Application US/10315964A
; Publication No. US20030148956A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert J
; APPLICANT: Mazur, Wieslaw A
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists
; FILE REFERENCE: 8847M3
; CURRENT APPLICATION NUMBER: US/10/315,964A
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US 60/349,117
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/376,337
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/388,895
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/411,988
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 530
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 114
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized artificial peptide
; NAME/KEY: MOD RES
; LOCATION: (38)..(38)
; OTHER INFORMATION: AMIDATION
US-10-315-964A-114

Query Match 25.1%; Score 140; DB 14; Length 38;
Best Local Similarity 76.3%; Pred. No. 7,7e-08;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 72 VIISLDVPIGLRIILBOARKYKARNOATNAQIIAHV 109
DB 1 IVISLDVPIGLRIILBOARKYKARNOATNAQIIAHV 38

RESULT 9
US-10-317-251A-114
; Sequence 114, Application US/10317251A
; Publication No. US20030148957A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert J
; APPLICANT: Mazur, Wieslaw A
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists
; FILE REFERENCE: 8847M2
; CURRENT APPLICATION NUMBER: US/10/317,251A
; CURRENT FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: US 60/349,117
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/376,337
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/388,895
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/411,988
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 530
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 114
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized artificial peptide
US-10-317-251A-114

QY 72 VIISLDVPIGLRIILBOARKYKARNOATNAQIIAHV 110
DB 1 IVISLDVPIGLRIILBOARKYKARNOATNAQIIAHV 39

NAME/KEY: MOD RES
LOCATION: (38)
OTHER INFORMATION: AMIDATION
US-10-317-251A-114

Query Match 25.1%; Score 140; DB 14; Length 38;
Best Local Similarity 76.3%; Pred. No. 7.7e-08;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 72 VILSDVPILGLRLLEQARYKARNQATNAQILAHV 109
DB 1 IVLSIDVPILGLRLLEQARARAREQATTNARILARV 38

RESULT 10

US-10-317-252A-114
Sequence 114, Application US/10317252A
Publication No. US20030148956A1
GENERAL INFORMATION:
APPLICANT: The Procter & Gamble Company
APPLICANT: Isfort, Robert J
APPLICANT: Mazur, Wieslaw A
TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists
FILE REFERENCE: 8847M
CURRENT APPLICATION NUMBER: US/10/317,252A
CURRENT FILING DATE: 2003-03-31
PRIOR APPLICATION NUMBER: US 60/349,117
PRIOR FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: US 60/376,337
PRIOR FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: US 60/388,895
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: US 60/411,988
PRIOR FILING DATE: 2002-09-19
NUMBER OF SEQ ID NOS: 530
SOFTWARE: PatentIn version 3.2
SEQ ID NO 114
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Chemically synthesized artificial peptide
FEATURE:
NAME/KEY: MOD RES
LOCATION: (38)
OTHER INFORMATION: AMIDATION
US-10-317-252A-114

Query Match 25.1%; Score 140; DB 14; Length 38;
Best Local Similarity 76.3%; Pred. No. 7.7e-08;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 72 VILSDVPILGLRLLEQARYKARNQATNAQILAHV 109
DB 1 IVLSIDVPILGLRLLEQARARAREQATTNARILARV 38

RESULT 11
US-09-919-473-4
Sequence 4, Application US/09919473
Patent No. US20020127221A1
GENERAL INFORMATION:
APPLICANT: Vale, Wylie Walker Jr.
APPLICANT: Lewis, Kathy Ann
APPLICANT: Reyes, Teresa Marie
APPLICANT: Hogenesch, John Beren
APPLICANT: Sawchenko, Paul Emil
APPLICANT: Vaughan, Joan Maureen
APPLICANT: Rivier, Jean Edward Frederic
APPLICANT: Pettin, Marilyn Heller
TITLE OF INVENTION: Orocortin Proteins and Uses Thereof
FILE REFERENCE: D6334
CURRENT APPLICATION NUMBER: US/09/919,473

CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/273,969
PRIOR FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 4
LENGTH: 38
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Amino acids 1-38 of human
OTHER INFORMATION: Orocortin-related peptide (hURP)
US-09-919-473-4

Query Match 25.0%; Score 139; DB 9; Length 38;
Best Local Similarity 76.3%; Pred. No. 9.8e-08;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 72 VILSDVPILGLRLLEQARYKARNQATNAQILAHV 109
DB 1 IVLSIDVPILGLRLLEQARARAREQATTNARILARV 38

RESULT 12
US-09-799-978-44
Sequence 44, Application US/09799978
Publication No. US20030165807A1
GENERAL INFORMATION:
APPLICANT: The Procter & Gamble Company
APPLICANT: Isfort, Robert
APPLICANT: Sheldon, Russell
TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or
TITLE OF INVENTION: Function Using Corticotropin Releasing Factor Receptors
FILE REFERENCE: 8448
CURRENT APPLICATION NUMBER: US/09/799,978
CURRENT FILING DATE: 2001-03-06
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.0
SEQ ID NO 44
LENGTH: 38
TYPE: PRT
ORGANISM: Homo sapiens
US-09-799-978-44

Query Match 25.0%; Score 139; DB 10; Length 38;
Best Local Similarity 76.3%; Pred. No. 9.8e-08;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 72 VILSDVPILGLRLLEQARYKARNQATNAQILAHV 109
DB 1 IVLSIDVPILGLRLLEQARARAREQATTNARILARV 38

RESULT 13
US-10-099-766-8
Sequence 8, Application US/10099766
Publication No. US20030036507A1
GENERAL INFORMATION:
APPLICANT: Lewis, Kathy
APPLICANT: Vale, Wylie
APPLICANT: Marlyn H Pettin
APPLICANT: Jean E. Rivier
APPLICANT: Koichi S. Kunitake
APPLICANT: Jozsef Guliyas
TITLE OF INVENTION: Orocortin III and Uses Thereof
FILE REFERENCE: D6390
CURRENT APPLICATION NUMBER: US/10/099,766
CURRENT FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/276,069
PRIOR FILING DATE: 2001-03-15
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 8
LENGTH: 38
TYPE: PRT

Wed Apr 21 12:21:13 2004

us-09-919-473-10.rapb

Page 5

ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human urocortin-related peptide (hURP),
OTHER INFORMATION: human urocortin II
US-10-099-766-8

Query Match 25.0%; Score 139; DB 14; Length 38;
Best Local Similarity 76.3%; Pred. No. 9.8e-08;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 72 VILSDVPVIGLRLLEQARYKARQAATNQAIIAHV 109
DB 1 IVLSLDVPIGLQLLEQARARAREQATTNARIARV 38

RESULT 14
US-10-315-964A-4
Sequence 4, Application US/10315964A
Publication No. US20030148956A1
GENERAL INFORMATION:
APPLICANT: The Procter & Gamble Company
APPLICANT: Isfort, Robert J
APPLICANT: Mazur, Wieslaw A
TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists
FILE REFERENCE: 8847M3
CURRENT APPLICATION NUMBER: US/10/315,964A
CURRENT FILING DATE: 2003-04-01
PRIOR APPLICATION NUMBER: US 60/349,117
PRIOR FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: US 60/376,337
PRIOR FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: US 60/388,895
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: US 60/411,988
PRIOR FILING DATE: 2002-09-19
NUMBER OF SEQ ID NOS: 530
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 38
TYPE: PRT
ORGANISM: Homo sapiens
US-10-315-964A-4

Query Match 25.0%; Score 139; DB 14; Length 38;
Best Local Similarity 76.3%; Pred. No. 9.8e-08;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 72 VILSDVPVIGLRLLEQARYKARQAATNQAIIAHV 109
DB 1 IVLSLDVPIGLQLLEQARARAREQATTNARIARV 38

RESULT 15
US-10-315-964A-123
Sequence 123, Application US/10315964A
Publication No. US20030148956A1
GENERAL INFORMATION:
APPLICANT: The Procter & Gamble Company
APPLICANT: Isfort, Robert J
APPLICANT: Mazur, Wieslaw A
TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists
FILE REFERENCE: 8847M3
CURRENT APPLICATION NUMBER: US/10/315,964A
CURRENT FILING DATE: 2003-04-01
PRIOR APPLICATION NUMBER: US 60/349,117
PRIOR FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: US 60/376,337
PRIOR FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: US 60/388,895
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: US 60/411,988
PRIOR FILING DATE: 2002-09-19
NUMBER OF SEQ ID NOS: 530

SOFTWARE: PatentIn version 3.2
SEQ ID NO 123
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Chemically synthesized artificial peptide
NAME/KEY: MOD_RES
LOCATION: (38)..(38)
OTHER INFORMATION: AMIDATION
US-10-315-964A-123

Query Match 25.0%; Score 139; DB 14; Length 38;
Best Local Similarity 76.3%; Pred. No. 9.8e-08;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 72 VILSDVPVIGLRLLEQARYKARQAATNQAIIAHV 109
DB 1 IVLSLDVPIGLQLLEQARARAREQATTNARIARV 38

Search completed: April 20, 2004, 19:06:53
Job time : 89.4933 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 20, 2004, 18:51:47 ; Search time 53.76 Seconds

(without alignments)
657.330 Million cell updates/sec

Title: US-09-919-473-10

Sequence: 1 MTRWALVVFVYMLDRILFY.....KARNQAATNAQTIAHVGR 112

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

SPTRMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriopl:*

17: sp_archaeop:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	117	21.0	151	13	0918B5
2	89.5	16.1	157	5	091KX2
3	84.5	15.2	499	5	091UE1
4	81	14.5	119	5	091PT0
5	80.5	14.5	649	11	08BKD5
6	80.5	14.5	1450	11	080T94
7	79.5	14.2	187	11	08CITO
8	79	14.2	338	3	042882
9	78.5	14.1	603	4	09H6V7
10	78.5	14.1	920	4	09H3X4
11	78.5	14.1	924	4	09HVI9
12	78.5	14.1	924	4	09H763
13	78.5	14.1	924	4	08WUB6
14	78.5	14.1	1409	4	09COA6
15	77.5	13.9	889	2	09X6X6
16	77.5	13.9	889	16	087NH2

17	77.5	13.9	889	16	082563	082563 salmonella
18	77.5	13.9	889	16	083T68	083T68 salmonella
19	76.5	13.7	592	12	08NRG2	08NRG2 cornebacte
20	76.5	13.7	699	11	0920T5	0920T5 mus musculu
21	76.5	13.7	751	11	09R218	09R218 mus musculu
22	76	13.6	542	3	09URQ4	09URQ4 saccharomyc
23	76	13.6	579	5	081IC6	081IC6 drosophila
24	75.5	13.6	1337	1	09Y818	09Y818 thermococcu
25	75.5	13.6	2093	4	015010	015010 homo sapien
26	75.5	13.5	2119	4	086X03	086X03 homo sapien
27	75	13.5	195	5	08B1H2	08B1H2 anophelae g
28	75	13.5	346	8	08SHH6	08SHH6 chameleleo e
29	75	13.5	1286	8	0841Q2	0841Q2 bacillus gl
30	74.5	13.4	756	5	044418	044418 chironomus
31	74.5	13.4	756	5	044417	044417 chironomus
32	73.5	13.2	164	4	014851	014851 homo sapien
33	73.5	13.2	506	5	086KV8	086KV8 dictyosteli
34	73.5	13.2	712	4	08H5C8	08H5C8 homo sapien
35	73.5	13.2	2344	5	086H67	086H67 dictyosteli
36	73.5	13.2	22152	4	08WX17	08WX17 homo sapien
37	73	13.1	125	17	09Y940	09Y940 aeropyrum p
38	73	13.1	528	3	0874N8	0874N8 candida gl
39	73	13.1	802	16	09A511	09A511 calobacter
40	72.5	13.0	232	16	083JR1	083JR1 shigella fl
41	72.5	13.0	526	2	085316	085316 salmonella
42	72.5	13.0	803	5	086J08	086J08 dictyosteli
43	72.5	13.0	1496	4	092626	092626 homo sapien
44	72.5	13.0	1983	5	09U165	09U165 leishmania
45	72.5	13.0	3283	16	0821S2	0821S2 salmonella

ALIGNMENTS

RESULT 1	ID	0918B5	PRELIMINARY:	PRT:	151 AA.
AC	0918B5	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	Urococtin precursor.				
GN	UCN.				
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;				
OC	Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;				
OC	Tetraodontidae; Tetraodontidae; Takifugu.				
OX	NCBI TaxID=31033;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20485066; PubMed=11032317;				
RA	Brunner B., Gruetznr F., Yaspo M.L., Ropers H.H., Haaf T.,				
RA	Kalscheuer V.M.;				
RT	Molecular cloning and characterization of the Fugu rubripes				
RT	MSR/COP2 imprinting cluster and chromosomal localization in Fugu and				
RT	Tetraodon nigroviridis."				
RL	Chromosome Res. 8:465-476 (2000).				
DR	EMBL: AJ251323; CAB96535.1; --.				
KM	Signal.				
FT	1				
ST	SEQUENCE				
SQ	151 AA; 16686 MW; EEBID52C41A67124 CRC64;				
Query Match	21.0%; Score 117; DB 13; Length 151;				
Best Local Similarity	33.3%; Pred. No. 8.9e-05;				
Matches	36; Conservative 21; Mismatches 31; Indels 20; Gaps 4;				
CY	20 VPG-TPIPTFOLLPOUSLETPSVTSSESSGTTTPPSM-----SNGTA 64				
DB	48 VPQYSPADWDVASTLQSAV--LSSSSAESSRKRTPAFAFYRFLRFTKRGQMLRVSXG 104				
CY	65 SPVLDKRVILSDVPIGLRLILDCARYKARNQAATNAQTIAHVGR 112				

Db 105 D--RRSRLTSLSDVPTNINWLVFDVAKAKNTLAKAENARLLAHIGRR 150

RESULT 2
Q9WIK2 PRELIMINARY; PRT; 157 AA.
AC Q9WIK2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE CG12491 protein.
GN CG12491.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Borchan M.R., Bouck J., Brockstein P., Brotler P.,
RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA Fowler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegam C.,
RA Jaitani W., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mostreft A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclet J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Teetor C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri U.S., Zhan W., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
DR EMBL; AF003461; AAF47056.1; -
DR FlyBase; FBgn0034900; CG12491.
SQ SEQUENCE 157 AA; 16832 MW; DD27BBB4827E914 CRC64;

Query Match 16.1%; Score 89.5; DB 5; Length 157;
Best Local Similarity 33.3%; Pred. No. 0.092;
Matches 27; Conservative 13; Mismatches 40; Indels 1; Gaps 1;

QY 32 PONSLETPSSVTSSESSGTTTGPASWSNSKAPYLDRVILSLVPTGILRLLEQAR 91
DB 73 PSSSSSTSPSSSSTSSSTATTTTPSSSDTSSSSSTSSDSSEYVRLRLRLRLRQR 131
QY 92 YKARNQATNQAIIAHVGR 112

Db 132 RCEIRREROEROERQQRAGRR 152

RESULT 3
Q9VEI PRELIMINARY; PRT; 499 AA.
AC Q9VEI;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE CG5043 protein.
GN CG5043.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Borchan M.R., Bouck J., Brockstein P., Brotler P.,
RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA Fowler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegam C.,
RA Jaitani W., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mostreft A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclet J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Teetor C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri U.S., Zhan W., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
DR EMBL; AF003465; AAF53609.1; -
DR FlyBase; FBgn0032636; CG5043.
SQ SEQUENCE 499 AA; 57015 MW; 564A3D68F447FD3 CRC64;

Query Match 15.2%; Score 84.5; DB 5; Length 499;
Best Local Similarity 30.2%; Pred. No. 1.4;
Matches 29; Conservative 17; Mismatches 29; Indels 21; Gaps 4;

QY 29 QLLPONSLETPSSVTSSESSGTTTGPASWSNSKAS-----PYL-----DFEVL 74
DB 64 QKIPETGLTTPSSSDNLTITGSSSGSSGSAKNTSLNEPSTRTYLLKXQQISTLI 123
QY 75 SLDPVIGLRLLEQARYKARNQATNQAIIAHVG 110

DB 124 NFRV-----RKSLSQMDPKFARRTG--NYQLVAHV 152

RESULT 4

Q9VPT0 PRELIMINARY; PRT; 119 AA.

AC Q9VPT0; 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)

DE CG13947 protein.

GN CG13947.

OS Drosophila melanogaster (fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Euphyptera; Endopterygota; Diptera; Brachycera; Muscomorpha; OX Ephypteroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkeley;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton R.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazer V.G., Chame M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.W., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotier P., Butts B.C., Buzam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo P., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fowler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Houston D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jatala M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kei Z., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Matei B., McIntosh T.C., McLeod M.P., McPherson P., Mekhlov G., Mlehnina N.V., Mobarry C., Morris A., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Paclio J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spter E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yen R.-F., Zaveri J.S., Zhao W., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of *Drosophila melanogaster*."

RL Science 287:2185-2195(2000).

DR EMBL; AEO03588; AAF51462.1;

DR FlyBase; FBgn0031277; CG13947.

SO SEQUENCE 119 AA; 10924 MW; 7036DA38659CA43C CRC64;

Query Match 14.5%; Score 81; DB 5; Length 119;

Best Local Similarity 47.8%; Pred. No. 0.54;

Matches 22; Conservative 5; Mismatches 15; Indels 4; Gaps 2;

QY 21 PGPPIPTFOLLIPONLETPPSVTSSESSSGTTTGSASNSK 64

DB 76 PGGFWGJLPPNATLPNSSTTTTSTTSTSTT--EASTSSPA 119

RESULT 5

Q8BKD5 PRELIMINARY; PRT; 649 AA.

AC Q8BKD5; 01-MAR-2003 (TREMBlrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE PLACE400063 protein homolog.

GN 2900045N06RIK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Eye;

RX MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium,

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."

RL Nature 420:563-573(2002).

DR EMBL; AK053541; BAC35420.1;

DR MGI; MGI:1920145; 2900045N06RIK.

SO SEQUENCE 649 AA; 68981 MW; CEP3A3C76B4496610 CRC64;

Query Match 14.5%; Score 80.5; DB 11; Length 649;

Best Local Similarity 28.3%; Pred. No. 5.3;

Matches 34; Conservative 12; Mismatches 41; Indels 33; Gaps 5;

QY 21 PGPPIPTFOLLIPONLETPPSVTSSESSSGTTT--PSASWSNSKASP----- 66

DB 509 PAHVPSTSLA---FTGTPGVSSQPHSGNSTGNLPRSCSSAAPTQGPSPDPTS 565

QY 67 ----YLDPRVILSL-----DVPIGLRLIL-----EQAYKARNOATTAQILAHVG 110

DB 566 DEVSSSTGTLSTSTPQNSRSLSPSDRLTSLPNAQSAAYQASRVASVNSQHPHRRG 625

RESULT 6

Q8OT94 PRELIMINARY; PRT; 1450 AA.

AC Q8OT94; 01-JUN-2003 (TREMBlrel. 24, Created)

DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE MKIAA1757 protein (Fragment).

GN MKIAA1757.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=N2579291; PubMed=12693553;

RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S., Nakajima D., Nagase T., Ohara O., Koga H.;

RT "Prediction of the coding sequences of mouse homologues of KIAA gene: RT cDNAs identified by screening of 400 mouse KIAA-homologous RT randomly sampled from size-fractionated libraries."

RL DNA Res. 10:35-48(2003).

DR EMBL; AK122551; BAC65833.1; --

DR InterPro; IPR001214; SET.

DR Pfam; PF00856; SET; 1.

DR SMART; SM00317; SET; 1.

DR PROSITE; PS00280; SET; 1.

FT NON TER 1

SO SEQUENCE 1450 AA; 158350 MW; 320136D1BC4C45B CRC64;

QY Query Match 14.5%; Score 80.5; DB 11; Length 1450;

Best Local Similarity 28.3%; Pred. No. 15;

Matches 34; Conservative 12; Mismatches 41; Indels 33; Gaps 5;

QY 21 PGTPIPTFOLLFONSLTTPSSVTSSSSGTTTG---PSAWSNSKASPY----- 66
 DB 1310 PAHPVSTDSLAP---FTGTPGYSSQPHSGNSGTLPRRSCSSAASPPTQGPSDSPTS 1366
 QY 67 -----YLDTRVILSL-----DVPGLRLRL-----EQARYKAAANOATNAQILAHVG 110
 DB 1367 DSVGSSTGTLSSTFPONSRSLSLPSDLRTISLPSAGSAAVQASRVASVNSQHYPRHG 1426

RESULT 7

OCBITO PRELIMINARY; PRT; 187 AA.
 ID 08CITO
 AC 08CITO
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Preprocorticotropin-releasing hormone.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/c;
 RA Seasholtz A.F., Bourbonnais F.J., Harnden C.E., Camper S.A.;
 RT "Nucleotide Sequence and Expression of the Mouse Corticotropin-
 Releasing Hormone Gene";
 RL Mol. Cell. Neurosci. 2:266-273(1991).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/c;
 RA Seasholtz A.F., Bourbonnais F.J., Harnden C.E., Camper S.A.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY12673; AAN07905.1; -
 DR GO; GO:0005576; Cerebellar; IEA.
 DR GO; GO:0005179; P hormone activity; IEA.
 DR InterPro; IPR00187; corticotropin.
 DR InterPro; IPR003620; Urocortin_CRF.
 DR Pfam; PF00473; CRF; 1.
 DR PRINTS; PR01612; CRFPAMILY.
 DR PRODOM; PD005970; Urocortin_CRF; 1.
 DR SMART; SM00039; CRF; 1.
 DR PROSITE; PS00511; CRF; 1.
 RN CHAIN 187
 FT CHAIN 187
 SQ SEQUENCE 187 AA; 20778 MW; 55165291FAA998 CRC64;

Query Match 14.3%; Score 79.5; DB 11; Length 187;
 Best Local Similarity 28.9%; Pred. No. 1.4;
 Matches 24; Conservative 17; Mismatches 33; Indels 9; Gaps 2;

QY 31 LPONLET--TPSSVTSSSSGTTGPSASNSKASPYLDTRVILSLDVPGLRLRL 88
 DB 112 MFORLSDSAEPAERGAEDALGQALEREHRESEPP-----ISLDLTFHLREYLE 164

QY 89 QARYKAAANOATNAQILAHVG 111
 DB 165 MARAEQLAQASHNRKMLWEITGX 187

RESULT 8

OCBITO PRELIMINARY; PRT; 338 AA.
 ID 042882
 AC 042882
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.

OX NCBI_TaxID=4896;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972h-;
 RA McLean J., Harris D., Wood V., Barrell B.G., Ralandream M.A.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL021817; CA11026.1; -
 DR PIR; T39159; T39159
 DR GeneDB_Spombe; SPAC8E11.05c; -
 RN Hypothetical protein.
 SQ SEQUENCE 338 AA; 38200 MW; 252D3319E127C6BF CRC64;

Query Match 14.2%; Score 79; DB 3; Length 338;
 Best Local Similarity 27.7%; Pred. No. 3.4;
 Matches 28; Conservative 9; Mismatches 28; Indels 36; Gaps 3;

QY 8 VFTVLMIDLRLFYGPPIPTFOLLFONSLTTPSSVTSSSSGTTGPSASNSKASPY 67
 DB 202 IFVLTW-----GHPVLDLRLP-----TPSTGSPNSRTTLELSVTLPSKSEDEPY 247

QY 68 LDTTRVILSLDVPGLRLRLBOARYKAAANOATNAQILAH 108
 DB 248 LD-----YSAARLCSINRDALTH 266

RESULT 9

OCBITO PRELIMINARY; PRT; 603 AA.
 ID 09H6V7
 AC 09H6V7
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Hypothetical protein FLJ21825.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
 RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
 RT "NDO human cDNA sequencing project."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK025478; BAB1514.1; -
 RN Hypothetical protein.
 SQ SEQUENCE 603 AA; 63563 MW; 1CA4AEBCA9F83D50 CRC64;

Query Match 14.1%; Score 78.5; DB 4; Length 603;
 Best Local Similarity 28.3%; Pred. No. 8;
 Matches 34; Conservative 12; Mismatches 41; Indels 33; Gaps 5;

QY 21 PGTPIPTFOLLFONSLTTPSSVTSSSSGTTTG---PSAWSNSKASPYL----- 68
 DB 463 PAHPVSTDSLAP---FTGTPGYSSQPHSGNSGTLPRRSCSSAASPPTQGPSDSPTS 519

QY 69 -----DTRVILSL-----DVPGLRLRL-----EQARYKAAANOATNAQILAHVG 110
 DB 520 DSVGSSTGTLSSTFPONSRSLSLPSDLRTISLPSAGSAAVQASRVASVNSQHYPRHG 579

RESULT 10

OCBITO PRELIMINARY; PRT; 920 AA.
 ID 09H3X4
 AC 09H3X4
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=amygdala;
RA Koehrer K., Beyer A., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RW EMBL; AL442073; CAC09439.1; -
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 920 AA; 98580 MW; 5E65FF2686511DAC CRC64;

Query Match 14.1%; Score 78.5; DB 4; Length 920;
Best Local Similarity 28.3%; Pred. No. 14;
Matches 34; Conservative 12; Mismatches 41; Indels 33; Gaps 5;

QY 21 PGPIPTFOLLQNSLETTPSSVTSSSGTTTG---PSASWSNKSAPYL----- 68
Db 780 PAHPVSTDSLAP---FTGTPGVFSQPHSGNSTGSLPRSCPSAAASPTLQGPSDSPTS 836
QY 69 -----DTRVILSL-----DVPGLRLILL-----EQARYKAARNQAATNAQILAHVG 110
Db 837 DSVSQSSTGTLSTSPFQNSRSLPSDLRTISLPSAGQSAVYQASRVSAVNSQHYPHRG 896

RESULT 11
ID Q9NV19 PRELIMINARY; PRT; 924 AA.
AC Q9NV19;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ10707.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isegai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishii S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RL "NEDO human cDNA sequencing project.";
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RW EMBL; AK001569; BA91762.1; -
KW Hypothetical protein.
SQ SEQUENCE 924 AA; 99092 MW; 9EAC1C3D92A44CEE CRC64;

Query Match 14.1%; Score 78.5; DB 4; Length 924;
Best Local Similarity 28.3%; Pred. No. 14;
Matches 34; Conservative 12; Mismatches 41; Indels 33; Gaps 5;

QY 21 PGPIPTFOLLQNSLETTPSSVTSSSGTTTG---PSASWSNKSAPYL----- 68
Db 784 PAHPVSTDSLAP---FTGTPGVFSQPHSGNSTGSLPRSCPSAAASPTLQGPSDSPTS 840
QY 69 -----DTRVILSL-----DVPGLRLILL-----EQARYKAARNQAATNAQILAHVG 110
Db 841 DSVSQSSTGTLSTSPFQNSRSLPSDLRTISLPSAGQSAVYQASRVSAVNSQHYPHRG 900

RESULT 12
ID Q9H7S3 PRELIMINARY; PRT; 924 AA.
AC Q9H7S3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ14322.
OS Homo sapiens (Human)

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isegai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RW EMBL; AK024384; BAB14903.1; -
KW Hypothetical protein.
SQ SEQUENCE 924 AA; 99072 MW; 358150B216B8C881 CRC64;

Query Match 14.1%; Score 78.5; DB 4; Length 924;
Best Local Similarity 28.3%; Pred. No. 14;
Matches 34; Conservative 12; Mismatches 41; Indels 33; Gaps 5;

QY 21 PGPIPTFOLLQNSLETTPSSVTSSSGTTTG---PSASWSNKSAPYL----- 68
Db 784 PAHPVSTDSLAP---FTGTPGVFSQPHSGNSTGSLPRSCPSAAASPTLQGPSDSPTS 840
QY 69 -----DTRVILSL-----DVPGLRLILL-----EQARYKAARNQAATNAQILAHVG 110
Db 841 DSVSQSSTGTLSTSPFQNSRSLPSDLRTISLPSAGQSAVYQASRVSAVNSQHYPHRG 900

RESULT 13
ID Q8WUB6 PRELIMINARY; PRT; 924 AA.
AC Q8WUB6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RW EMBL; BC020956; AAH20956.1; -
KW Hypothetical protein.
SQ SEQUENCE 924 AA; 99082 MW; 9A3CC00E2537C99F CRC64;

Query Match 14.1%; Score 78.5; DB 4; Length 924;
Best Local Similarity 28.3%; Pred. No. 14;
Matches 34; Conservative 12; Mismatches 41; Indels 33; Gaps 5;

QY 21 PGPIPTFOLLQNSLETTPSSVTSSSGTTTG---PSASWSNKSAPYL----- 68
Db 784 PAHPVSTDSLAP---FTGTPGVFSQPHSGNSTGSLPRSCPSAAASPTLQGPSDSPTS 840
QY 69 -----DTRVILSL-----DVPGLRLILL-----EQARYKAARNQAATNAQILAHVG 110
Db 841 DSVSQSSTGTLSTSPFQNSRSLPSDLRTISLPSAGQSAVYQASRVSAVNSQHYPHRG 900

RESULT 14
ID Q9C0A6 PRELIMINARY; PRT; 1409 AA.
AC Q9C0A6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein KIAA1757 (Fragment).
GN KIAA1757.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=21082932; PubMed=11214970;
RA Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIX.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro."
RL DNA Res. 7:347-355(2000).
CC -1- SIMILARITY: CONTAINS 1 SET DOMAIN.
EMBL: AB051544; BAB21848.1; --
DR InterPro; IPR001214; SET.
DR Pfam; PF00856; SET; 1.
DR SMART; SM00317; SET; 1.
DR PROSITE; PS0280; SET; 1.
DR KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 1409 AA; 154203 MW; B8ED7A94B6AC0606 CRC64;

Query Match 14.1%; Score 78.5; DB 4; Length 1409;
Best Local Similarity 28.3%; Pred. No. 23;
Matches 34; Conservative 12; Mismatches 41; Indels 33; Gaps 5;

QY 21 PGTPIPTQLLPQNSLETTPSSVTSESSSGTTG---PSASWSNSKASPYL----- 68
DB 1269 PAHPVSTDSLAP---FTGTGVFFSQPHSGNSGTSLPRRCPSSAASTLQGPSDSPTS 1325

QY 69 -----DTRVILSL-----DVPIGILRL-----EQARYKAARNOATNAQILAHVG 110
DB 1326 DSVSQSGTGTLSSTSPFPPNSRSLPSDLTSLPSAGOSAVYQASRVSAVNSQHYPHRG 1385

RESULT 15
QX6X6 PRELIMINARY; PRT; 889 AA.
AC Q9X6X6;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Putative regulator YojN.
GN YojN.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RA Siano M.A., Mariconda S.E., Harshey R.M.;
RT "Salmonella typhimurium homolog of YojN."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF153717; AAD34637.1; --
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR008207; Hpt.
DR Pfam; PFC02518; HATPase_c; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00073; HPT; 1.
DR PROSITE; PS0109; HIS_KIN; 1.
DR PROSITE; PS00894; HPT; 1.
SQ SEQUENCE 889 AA; 99795 MW; 4A10BD40EEC6D261 CRC64;

Query Match 13.9%; Score 77.5; DB 2; Length 889;
Best Local Similarity 26.4%; Pred. No. 17;
Matches 33; Conservative 18; Mismatches 39; Indels 35; Gaps 5;

QY 18 LFVFGPIPTFQLLP-----QNSLETTPTSSVTSE-----SSSGTTTGPSASWSNS 62

Db 238 LIPPCMPLDSFRIEDATQATGRSRSEKAPDSVTISFNGSKIEISSALNSTGMELINQVP 297
QY 63 KASPYLDT--RVILSLDVPIGILRL-----EQARYKAARNO-----AATN 102
DB 298 FTLLDLDLQNLILLPLLNIGLLALPFGYATFRHQPGRSTESTSGNANNEELRVLRIN 357
QY 103 AQILA 107
DB 358 EIVS 362

Search completed: April 20, 2004, 18:56:42
Job time : 55.76 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	179	32.1	38	4	US-09-799-978-43	Sequence 43, Appl
2	139	25.0	38	4	US-09-799-978-44	Sequence 44, Appl
3	76	13.6	542	4	US-09-189-462-6	Sequence 6, Appl
4	76	13.6	542	4	US-09-863-040-6	Sequence 6, Appl
5	72.5	13.0	526	2	US-08-863-659A-40	Sequence 40, Appl
6	71.5	12.8	308	4	US-09-252-991A-32516	Sequence 40, Appl
7	71.5	12.8	410	4	US-09-252-991A-30606	Sequence 32516, A
8	71.5	12.8	485	1	US-08-471-496-9	Sequence 9, Appl
9	71.5	12.8	485	2	US-08-894-840-9	Sequence 9, Appl
10	71.5	12.8	485	3	US-09-139-675-9	Sequence 9, Appl
11	71.5	12.8	465	4	US-08-502-018-9	Sequence 9, Appl
12	71.5	12.8	521	1	US-08-063-552-2	Sequence 2, Appl
13	71.5	12.8	521	5	PCT-US93-05704-2	Sequence 2, Appl
14	71	12.7	422	4	US-09-252-991A-30314	Sequence 30314, A
15	70.5	12.7	1069	4	US-09-252-991A-24533	Sequence 24533, A
16	70	12.6	275	2	US-08-578-709-13	Sequence 13, Appl
17	70	12.6	390	4	US-09-489-039A-13547	Sequence 13547, A
18	70	12.6	425	4	US-09-489-039A-11016	Sequence 11016, A
19	70	12.6	500	2	US-08-578-709-15	Sequence 15, Appl
20	69	12.4	696	4	US-09-907-7794A-91	Sequence 91, Appl
21	69	12.4	696	4	US-09-305-125A-91	Sequence 91, Appl
22	69	12.4	696	4	US-09-302-775A-91	Sequence 91, Appl
23	68.5	12.3	171	5	PCT-US95-04910-12	Sequence 12, Appl
24	68	12.2	124	3	US-08-381-189B-15	Sequence 15, Appl
25	68	12.2	1025	4	US-09-711-164-443	Sequence 443, App
26	67.5	12.1	582	3	US-08-906-865-3	Sequence 3, Appl
27	67.5	12.1	582	4	US-09-429-668-3	Sequence 3, Appl

Query Match 25.0%; Score 139; DB 4; Length 38;
Best Local Similarity 76.3%; Pred. No. 1.2e-09;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 72 VILSDVIGLRLLEQARVKAARNOATQAIIAHV 109
DB 1 IYVLSLDVIGLRLLEQARARAREQATTNARIARV 38

RESULT 3

US-09-189-462-6

; Sequence 6, Application US/09189462

; Patent No. 6303302

; GENERAL INFORMATION:

; APPLICANT: Rupp, Steffan

; APPLICANT: Robertson, Laura

; APPLICANT: Summers, Eric F.

; APPLICANT: Hecht, Peter

; APPLICANT: Roberts, Radclyffe

; APPLICANT: Madhani, Hiren

; APPLICANT: Styles, Cora Ann

; APPLICANT: Lo, Hsiu-Jung

; APPLICANT: Sherman, Amir

; APPLICANT: Cali, Brian

; APPLICANT: Pink, Gerald

; TITLE OF INVENTION: REGULATION OF FUNGAL GENE EXPRESSION
; FILE REFERENCE: 50078/003002
; CURRENT APPLICATION NUMBER: US/09/189,462
; CURRENT FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/066,129
; EARLIER FILING DATE: 1997-11-19
; EARLIER APPLICATION NUMBER: 60/066,308
; EARLIER FILING DATE: 1997-11-21
; EARLIER APPLICATION NUMBER: 60/066,462
; EARLIER FILING DATE: 1997-11-24
; EARLIER APPLICATION NUMBER: 60/078,610
; EARLIER FILING DATE: 1998-03-19
; EARLIER APPLICATION NUMBER: 60/094,523
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; TYPE: PRT
; LENGTH: 542
; ORGANISM: Saccharomyces cerevisiae

US-09-189-462-6

Query Match 13.6%; Score 76; DB 4; Length 542;
Best Local Similarity 40.0%; Pred. No. 1.5;
Matches 18; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

OY 35 SLETTPTSSVTSSSGTTTGPSASNSKASPYLDTRVILSDVP 79
DB 226 STEDESSSYTQITQKSTTSSNSSSSVNSKTSPLPKNTVTISVDIP 270

RESULT 4

US-09-863-040-6

; Sequence 6, Application US/09863040

; Patent No. 6599705

; GENERAL INFORMATION:

; APPLICANT: Rupp, Steffan

; APPLICANT: Robertson, Laura

; APPLICANT: Summers, Eric F.

; APPLICANT: Hecht, Peter

; APPLICANT: Roberts, Radclyffe

; APPLICANT: Madhani, Hiren

; APPLICANT: Styles, Cora Ann

; APPLICANT: Lo, Hsiu-Jung

; APPLICANT: Sherman, Amir

; APPLICANT: Cali, Brian

; APPLICANT: Pink, Gerald R.

; TITLE OF INVENTION: Regulation of Fungal Gene Expression

; FILE REFERENCE: 109272.152

; CURRENT APPLICATION NUMBER: US/09/863,040

; CURRENT FILING DATE: 2001-05-22

; PRIOR APPLICATION NUMBER: US 60/066,129

; PRIOR FILING DATE: 1997-11-19

; PRIOR APPLICATION NUMBER: US 60/066,308

; PRIOR FILING DATE: 1997-11-21

; PRIOR APPLICATION NUMBER: US 60/066,462

; PRIOR FILING DATE: 1997-11-24

; PRIOR APPLICATION NUMBER: US 60/078,610

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: US 60/094,523

; PRIOR FILING DATE: 1998-07-29

; NUMBER OF SEQ ID NOS: 67

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6

; LENGTH: 542

; TYPE: PRT

; ORGANISM: Saccharomyces cerevisiae INV9

; US-09-863-040-6

Query Match 13.6%; Score 76; DB 4; Length 542;
Best Local Similarity 40.0%; Pred. No. 1.5;
Matches 18; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

OY 35 SLETTPTSSVTSSSGTTTGPSASNSKASPYLDTRVILSDVP 79
DB 226 STEDESSSYTQITQKSTTSSNSSSSVNSKTSPLPKNTVTISVDIP 270

RESULT 5

US-08-853-659A-40

; Sequence 40, Application US/08853659A

; Patent No. 5935522

; GENERAL INFORMATION:

; APPLICANT: Wong, K.K.; Saffer, J.D.

; TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection

; TITLE OF INVENTION: Of A

; TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella

; NUMBER OF SEQUENCES: 67

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Paul W. Zimmerman

; ADDRESSEE: Intellectual Property Services

; ADDRESSEE: Battelle Memorial Institute

; ADDRESSEE: PNNL P.O. Box 999

; STREET: Washington Way

; CITY: Richland

; STATE: Washington

; COUNTRY: U.S.A.

; ZIP: 99352

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage

; COMPUTER: IBM PC/XT/AT

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: Word Processor (WordPerfect 5.1)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/853,659A

; FILING DATE: Unknown

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: none

; FILING DATE: n/a

; INFORMATION FOR SEQ ID NO: 40:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 526 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; US-08-853-659A-40

Query Match 13.0%; Score 72.5; DB 2; Length 526;
Best Local Similarity 29.2%; Pred. No. 3.8;
Matches 21; Conservative 14; Mismatches 22; Indels 15; Gaps 3;

QY 10 VLVMLDRILFVPGTPIPTFOLLPSNLETPSSVTSSSGTTTGPS---ASWSNSKASP 66
Db 162 LVITIDSV-----TDKTFELSPF-----SVSGHKGLTPTLTSTIVGTAEENAKVDI 209
QY 67 YLDRTRVILSLDV 78
Db 210 YVDNKLWASVDV 221

RESULT 6
US-09-252-991A-32516
; Sequence 32516, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: MARC J. RUBENFIELD et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32516

Query Match 12.8%; Score 71.5; DB 4; Length 308;
Best Local Similarity 35.6%; Pred. No. 2.4;
Matches 26; Conservative 11; Mismatches 27; Indels 9; Gaps 4;
QY 32 PONSLETPSSVTSSSGTTTGPSASWSNSKASPYLDTRVILSLDVPIGLRILLRQAR 91
Db 173 PISLEVCPSS--TSANTPTTALPSSTW-----LQDVLARRICASVRVP-SRTREMLGSPR 225
QY 92 YKAARNQATNAQ 104
Db 226 YH--QNIAGSTAQ 236

RESULT 7
US-09-252-991A-30606
; Sequence 30606, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: MARC J. RUBENFIELD et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30606

Query Match 12.8%; Score 71.5; DB 4; Length 410;
Best Local Similarity 27.0%; Pred. No. 3.5;
Matches 27; Conservative 13; Mismatches 37; Indels 23; Gaps 4;
QY 21 PGT--PIPT--FOLLPSNLETPSSVTSSSGTTTGPSASWSNSKASPYLDTRVILSLD 77

Db 9 PGDGPISPMFQQAPRGFLAAEPGAFAAAGAPVAAGVDAQVGIAGAPL----- 58
QY 78 VPIGLRILLRLEQA-----RYKAARNQATNAQIILAHV 109
Db 59 --VGLRRACIEPAVDAEGGFRYGRADHFGGGAQAQVLDHV 96

RESULT 8
US-08-471-496-9
; Sequence 9, Application US/08471496
; Patent No. 5798223
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; APPLICANT: CAO, LIANG
; APPLICANT: ROSEN, CRAIG
; TITLE OF INVENTION: HUMAN AMINE TRANSPORTER
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,496
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US95/02645
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0830001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 465 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-471-496-9

Query Match 12.8%; Score 71.5; DB 1; Length 465;
Best Local Similarity 33.3%; Pred. No. 4.2;
Matches 22; Conservative 8; Mismatches 25; Indels 11; Gaps 2;
QY 6 LVVFFVLMLEDRILFVPGTPI-PTFOLLPSNLETPSSVTSSSGTTTGPSASWSNSKA 64
Db 25 VVVEVALLDMLLTVVVPIVPTFLY-----ATEFKDSNSLHRGSPSVSQOALT 74
QY 65 SPYLDLT 70
Db 75 SPAFST 80

RESULT 9
US-08-894-840-9
; Sequence 9, Application US/08894840
; Patent No. 5859200
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; APPLICANT: CAO, LIANG
; APPLICANT: ROSEN, CRAIG A.

TITLE OF INVENTION: HUMAN AMINE TRANSPORTER
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,840
FILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0830000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 465 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-840-9

Query Match 12.8%; Score 71.5; DB 2; Length 465;
Best Local Similarity 33.3%; Pred. No. 4.2; Mismatches 25; Indels 11; Gaps 2;
Matches 22; Conservative 8;
QY 6 LVFVVLMLDRILFVPGTPI-PTFQLLPONSLETPSSVTSSESSGTTTGPASWSNSKA 64
Db 25 VVVFVALLDNMLLTVVVPVPTFLY-----ATEFKDSNSSLHSGPSVSSQALT 74
QY 65 SPYLDI 70
Db 75 SPAFST 80

RESULT 10
US-09-139-675-9
Sequence 9, Application US/09139675A
Patent No. 6117426
GENERAL INFORMATION:
APPLICANT: Li, Yi
APPLICANT: Cao, Liang
APPLICANT: Rosen, Craig
TITLE OF INVENTION: Human Amine Transporter
FILE REFERENCE: 1488.0830003
CURRENT APPLICATION NUMBER: US/09/139,675A
CURRENT FILING DATE: 1998-08-25
EARLIER APPLICATION NUMBER: WO PCT/US95/02645
EARLIER FILING DATE: 1995-03-01
EARLIER APPLICATION NUMBER: US 08/471,496
EARLIER FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 9
LENGTH: 465
TYPE: PRT
ORGANISM: Rattus sp.
US-09-139-675-9

Query Match 12.8%; Score 71.5; DB 3; Length 465;
Best Local Similarity 33.3%; Pred. No. 4.2; Mismatches 25; Indels 11; Gaps 2;
Matches 22; Conservative 8;

QY 6 LVFVVLMLDRILFVPGTPI-PTFQLLPONSLETPSSVTSSESSGTTTGPASWSNSKA 64
Db 25 VVVFVALLDNMLLTVVVPVPTFLY-----ATEFKDSNSSLHSGPSVSSQALT 74
QY 65 SPYLDI 70
Db 75 SPAFST 80
RESULT 11
US-09-502-018-9
Sequence 9, Application US/09502018
Patent No. 6630443
GENERAL INFORMATION:
APPLICANT: Li, Yi
APPLICANT: Rosen, Craig
APPLICANT: Cao, Liang
TITLE OF INVENTION: Human Amine Transporter
FILE REFERENCE: 1488.0830003
CURRENT APPLICATION NUMBER: US/09/502,018
CURRENT FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US/09/139,675
PRIOR FILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: WO PCT/US95/02645
PRIOR FILING DATE: 1995-03-01
PRIOR APPLICATION NUMBER: US 08/471,496
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 9
LENGTH: 465
TYPE: PRT
ORGANISM: Rattus sp.
US-09-502-018-9

Query Match 12.8%; Score 71.5; DB 4; Length 465;
Best Local Similarity 33.3%; Pred. No. 4.2; Mismatches 25; Indels 11; Gaps 2;
Matches 22; Conservative 8;
QY 6 LVFVVLMLDRILFVPGTPI-PTFQLLPONSLETPSSVTSSESSGTTTGPASWSNSKA 64
Db 25 VVVFVALLDNMLLTVVVPVPTFLY-----ATEFKDSNSSLHSGPSVSSQALT 74
QY 65 SPYLDI 70
Db 75 SPAFST 80

RESULT 12
US-08-063-552-2
Sequence 2, Application US/08063552
Patent No. 5688936
GENERAL INFORMATION:
APPLICANT: Edwards, Robert H
TITLE OF INVENTION: Vesicle Membrane Transport Proteins
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STATE: California
COUNTRY: USA
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/063,552
FILING DATE: 19930514
CLASSIFICATION: 530

```
ATTORNEY/AGENT INFORMATION:
; NAME: Farber, Michael B
; REGISTRATION NUMBER: 32,612
; REFERENCE/DOCKET NUMBER: 9067-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (818) 796-4000
; TELEFAX: (818) 795-6321
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 521 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-063-552-2
Query Match 12.8%; Score 71.5; DB 1; Length 521;
Best Local Similarity 33.3%; Pred. No. 4.9;
Matches 22; Conservative 8; Mismatches 25; Indels 11; Gaps 2;

Qy 6 LVFVVLMLDRILFVPGTPI-PTFQLLPQNSLETTPSSVTSSSGTTTGPASWSNSKA 64
Db 25 VVVFVALLDNNMLLTVVVIVPTFLY-----ATEFKDSNSLHGRGFSVSSQQALT 74

Qy 65 SPYLDY 70
Db 75 SPAFST 80

US-09-252-991A-30314
; SEQUENCE 30314, Application US/09252991A
; PATENT NO. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30314
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30314
Query Match 12.7%; Score 71; DB 4; Length 422;
Best Local Similarity 25.0%; Pred. No. 4.2;
Matches 19; Conservative 16; Mismatches 38; Indels 0; Gaps 0;

Qy 40 PSSVTSSSGTTTGPASWSNSKASPYLDTRVILSLDVPGLRLLEQARYKAARNQA 99
Db 11 PAATAAIPRAGATGCGGSGATGPRSMASRRSAELPVPELRQVARCQCCQQAEOAE 70

Qy 100 ATNAQILAHVGR 111
Db 71 QASARVLRHLDR 82

US-09-252-991A-24533
; SEQUENCE 24533, Application US/09252991A
; PATENT NO. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24533
; LENGTH: 1069
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24533
Query Match 12.7%; Score 70.5; DB 4; Length 1069;
Best Local Similarity 27.1%; Pred. No. 17;
Matches 39; Conservative 13; Mismatches 35; Indels 57; Gaps 7;

Qy 5 ALVVVVVLMRLDRILF-----VPGTPIPTFO---LLPQNSLETTPSSV----- 43
Db 52 ALLTASLLGLGLAFRLGVAPLPEADFTPIQNALPFGSPETMASSVATPLEVQPSAI 111

Qy 44 -----TSESSSGTTTGPASWSNSKA-----SPYLDY-RVIL 74
Db 25 VVVFVALLDNNMLLTVVVIVPTFLY-----ATEFKDSNSLHGRGFSVSSQQALT 74
```

```
ATTORNEY/AGENT INFORMATION:
; NAME: Farber, Michael B
; REGISTRATION NUMBER: 32,612
; REFERENCE/DOCKET NUMBER: 9067-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (818) 796-4000
; TELEFAX: (818) 795-6321
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 521 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-05704-2
Query Match 12.8%; Score 71.5; DB 5; Length 521;
Best Local Similarity 33.3%; Pred. No. 4.9;
Matches 22; Conservative 8; Mismatches 25; Indels 11; Gaps 2;

Qy 6 LVFVVLMLDRILFVPGTPI-PTFQLLPQNSLETTPSSVTSSSGTTTGPASWSNSKA 64
Db 25 VVVFVALLDNNMLLTVVVIVPTFLY-----ATEFKDSNSLHGRGFSVSSQQALT 74

Qy 65 SPYLDY 70
Db 75 SPAFST 80

PCT-US93-05704-2
; SEQUENCE 2, Application PC/TUS9305704
; GENERAL INFORMATION:
; APPLICANT: Edwards, Robert H
; TITLE OF INVENTION: Vesicle Membrane Transport Proteins
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, Ninth Floor
; CITY: Pasadena
; STATE: California
; COUNTRY: USA
; ZIP: 91001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05704
; FILING DATE: 19930611
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Farber, Michael B
; REGISTRATION NUMBER: 32,612
; REFERENCE/DOCKET NUMBER: 9067-1PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (818) 796-4000
; TELEFAX: (818) 795-6321
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 521 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-05704-2
Query Match 12.8%; Score 71.5; DB 5; Length 521;
Best Local Similarity 33.3%; Pred. No. 4.9;
Matches 22; Conservative 8; Mismatches 25; Indels 11; Gaps 2;

Qy 6 LVFVVLMLDRILFVPGTPI-PTFQLLPQNSLETTPSSVTSSSGTTTGPASWSNSKA 64
Db 25 VVVFVALLDNNMLLTVVVIVPTFLY-----ATEFKDSNSLHGRGFSVSSQQALT 74
```


Db 112 PGITEMTSSALGTTT-LTLOFSLDKSIDVAAQEVQAAINAAGRLPVDMENLPTWRKV 170
QY 75 SLDVPIGLRI-----ILEQARY 92
Db 171 PADSPIMILRVNSENMPLELSDY 194

Search completed: April 20, 2004, 18:58:16
Job time : 35.64 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 20, 2004, 18:51:32 ; Search time 14.9333 Seconds
(without alignments)
390.526 Million cell updates/sec

Title: US-09-919-473-10

Perfect score: 557

Sequence: 1 MTRKALVWFVLMRLILFV.....KAARNQATNAQILAHVRR 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141691 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141691

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	557	100.0	112	1	UCN2_MOUSE
2	482.5	86.6	109	1	UCN2_RAT
3	312	56.0	112	1	UCN2_HUMAN
4	100.5	18.0	164	1	UCN3_MOUSE
5	99	17.8	161	1	UCN3_HUMAN
6	79	14.2	539	1	STG2_HUMAN
7	76	13.6	837	1	MUCL_RAT
8	75.5	13.6	2090	1	N214_HUMAN
9	74.5	13.4	196	1	CRF_HUMAN
10	71.5	12.8	222	1	VV SV5
11	71.5	12.8	436	1	GM1_MOUSE
12	71.5	12.8	519	1	AB31_ARATH
13	71.5	12.8	521	1	VMY1_RAT
14	71	12.7	1367	1	AMTH_YEAST
15	70.5	12.7	392	1	RPP SV5
16	70.5	12.7	4377	1	ANK3_HUMAN
17	70	12.6	145	1	UR1_CARAU
18	70	12.6	500	1	PTG1_HUMAN
19	70	12.6	519	1	M2P2_HUMAN
20	69.5	12.5	187	1	CRF_RAT
21	69.5	12.5	636	1	YNR6_YEAST
22	69	12.4	539	1	STG2_MOUSE
23	68.5	12.3	324	1	NA2 RHIL0
24	68.5	12.3	395	1	PAT DROEQ
25	68.5	12.3	532	1	VAT_HUMAN
26	68.5	12.3	743	1	TFEE_HUMAN
27	68	12.2	122	1	UCN1_MOUSE
28	68	12.2	122	1	UCN1_RAT
29	68	12.2	124	1	UCN1_HUMAN
30	68	12.2	145	1	UR1_CYPCA
31	68	12.2	162	1	UR1 CATCO
32	68	12.2	165	1	UR1 ONCMY
33	68	12.2	254	1	YMH1_CABEL

34	68	12.2	469	1	VL2_HPVME
35	68	12.2	605	1	WSC4_YEAST
36	68	12.2	681	1	YDHE_SCHPO
37	68	12.2	830	1	PKN2_MYXXA
38	68	12.2	1025	1	YEGO_ECOLI
39	68	12.2	1609	1	FIG2_YEAST
40	67.5	12.1	536	1	YEN1_SCHPO
41	67.5	12.1	582	1	SYN2_HUMAN
42	67.5	12.1	750	1	CTPB_MYCLE
43	67.5	12.1	794	1	KI11_HUMAN
44	67	12.0	234	1	MAG8_HUMAN
45	67	12.0	417	1	GP61_HUMAN

ALIGNMENTS

RESULT 1	UCN2_MOUSE	STANDARD;	PRT;	112 AA.
ID	UCN2_MOUSE			
AC	Q99ML8;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Urocortin II precursor (Ucn II).			
GN	UCN2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RP	[1]			
RC	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/C.			
RX	MEDLINE=21126973; PubMed=11226328;			
RA	Reyes T.M., Lewis K., Perrin M.H., Kunitake K.S., Vaughan J.,			
RA	Arias C.A., Hogenesch J.B., Gulyas J., Rivier J., Vale W.W.,			
RA	Sawchenko P.E.;			
RT	"Urocortin II: A member of the corticotropin-releasing factor (CRF)			
RT	neuropeptide family that is selectively bound by type 2 CRF			
RT	receptors."			
RL	Proc. Natl. Acad. Sci. U.S.A. 98:2843-2848 (2001).			
CC	-I- FUNCTION: Suppress food intake, delays gastric emptying and			
CC	decreases heat-induced edema. Might represent an endogenous ligand			
CC	for maintaining homeostasis after stress (By similarity).			
CC	-I- SUBUNIT: Binds with high affinity to CRF receptors 2-alpha and 2-			
CC	beta (By similarity).			
CC	-I- SUBCELLULAR LOCATION: Secreted.			
CC	-I- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing			
CC	factor/urotensin I family.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AF331517; AAK16157.1; ..			
DR	MGI; 2176375; Ucn2.			
DR	GO; GO:0005576; C:extracellular; ISS.			
DR	GO; GO:0005102; P:receptor binding; ISS.			
DR	GO; GO:0006171; P:cAMP biosynthesis; ISS.			
DR	GO; GO:0007586; P:digestion; ISS.			
DR	GO; GO:0006950; P:response to stress; ISS.			
DR	Hormone; Amidation; Signal.			
FT	SIGNAL 1 19 POTENTIAL.			
FT	PROPEP 20 70 POTENTIAL.			
FT	CHAIN 72 112 UROCORTIN II.			
SQ	SEQUENCE 112 AA; 12179 MW; C871002CDA64FB7 CRC64;			
Query Match	100.0%; Score 557; DB 1; Length 112;			
Best Local Similarity	100.0%; Pred. No. 1.4e-46;			

Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MTRWLVVFWVLMRLDRILFVPGTPIPTFOLLQNSLETTPSSVTSSSSGTTTGPSASWS 60
DB 1 MTRWLVVFWVLMRLDRILFVPGTPIPTFOLLQNSLETTPSSVTSSSSGTTTGPSASWS 60

QY 61 NSKASPYLDTRVILSLDVPGLRILLEQARYKAARNOATNAQILAHVGR 112
DB 61 NSKASPYLDTRVILSLDVPGLRILLEQARYKAARNOATNAQILAHVGR 112

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RESULT 2

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UCN2_RAT STANDARD; PRT; 109 AA.
AC Q91W1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Urocortin II precursor (Ucn II)
GN UCN2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley; TISSUE-Midbrain;
RA Park J.H., Ju S.K., Lee M.K.;
RT "Cloning and analysis of tissue-specific mRNA expression of rat
RT urocortin II";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Suppress food intake, delays gastric emptying and
CC decreases heat-induced edema. Might represent an endogenous ligand
CC for maintaining homeostasis after stress (by similarity).
CC -!- SUBUNIT: Binds with high affinity to CRF receptors 2-alpha and 2-
CC beta (by similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC factor/urotensin I family.

```

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```

CC EMBL; AY044835; AAK98780.1; -.
CC GO; GO:0005576; C:extracellular; ISS.
CC GO; GO:0005102; F:receptor binding; ISS.
CC GO; GO:0006171; P:cAMP biosynthesis; ISS.
CC GO; GO:0007586; P:digestion; ISS.
CC GO; GO:0006950; P:response to stress; ISS.
CC InterPro; IPR000187; corticoliberin.
CC SMART; SM00039; CRF; 1.
CC SIGNAL 1 19 POTENTIAL.
CC PROPEP 20 67 POTENTIAL.
CC CHAIN 69 109 UROCORTIN II.
CC SEQUENCE 109 AA; 11922 MW; AAB246D8903ED83E CRC64;

```

Query Match 86.6%; Score 482.5; DB 1; Length 109;

Best Local Similarity 90.2%; Pred. NO. 1.7e-39;

Matches 101; Conservative 2; Mismatches 6; Indels 3; Gaps 1;

```

QY 1 MTRWLVVFWVLMRLDRILFVPGTPIPTFOLLQNSLETTPSSVTSSSSGTTTGPSASWS 60
DB 1 MTRWLVVFWVLMRLDR---VPGTPIPTFOLLQNVPTTPSSVSSESDTTTGPSASWS 57

QY 61 NSKASPYLDTRVILSLDVPGLRILLEQARYKAARNOATNAQILAHVGR 112
DB 58 NSKASPYLDTRVILSLDVPGLRILLEQARYKAARNOATNAQILAHVGR 109

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RESULT 3

```

UCN2_HUMAN STANDARD; PRT; 112 AA.
AC Q96RF3; Q9BUG0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Urocortin II precursor (Ucn II) (Stresscopin-related peptide)
DE (Urocortin-related peptide).
GN UCN2 OR SRP OR URP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21227098; PubMed=11329063;
RA Heu S.Y., Hsueh A.J.W.;
RT "Human stresscopin and stresscopin-related peptide are selective
RT ligands for the type 2 corticotropin-releasing hormone receptor.";
RL Nat. Med. 7:605-611(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Skin, and Uterus;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Rahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalick D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

```

```

CC -!- FUNCTION: Suppress food intake, delays gastric emptying and
CC decreases heat-induced edema. Might represent an endogenous ligand
CC for maintaining homeostasis after stress.
CC -!- SUBUNIT: Binds with high affinity to CRF receptors 2-alpha and 2-
CC beta.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC factor/urotensin I family.

```

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```

CC EMBL; AF320560; AAK52672.1; -.
CC EMBL; BC002647; AAH02647.2; -.
CC EMBL; BC022096; AAH22096.1; -.
CC MIN; 605902; -.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0005102; F:receptor binding; IPI.
CC GO; GO:0006171; P:cAMP biosynthesis; IEP.
CC GO; GO:0007586; P:digestion; NAS.
CC GO; GO:0006950; P:response to stress; NAS.

```

DR InterPro: IPE000187; corticoliberin.
 DR SMART; SW00039; CRF; 1.
 KW Hormone; Amidation; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT PROPEP 20 70 POTENTIAL.
 FT CHAIN 72 112 UROCORTIN III.
 SQ SEQUENCE 112 AA; 12146 MW; 0EFF29A3463723D4 CRC64;
 Query Match 56.0%; Score 312; DB 1; Length 112;
 Best Local Similarity 60.9%; Pred. No. 3.5e-23;
 Matches 67; Conservative 15; Mismatches 28; Indels 0; Gaps 0;
 QY 1 MTRWLVVFWVLMRLIFVETGPIPTFQLLPQNSLETSSVTSSSTGTTTGPSASWS 60
 Db 1 MTRCALLLVLMGLRVLVWVPTPTFQLLPQNSLETSSVTSSSTGTTTGPSASWS 60
 QY 61 NSKASPVLDTRVILSLDVPGLILLLEQARYKARNOATNAQILAHVG 110
 Db 61 HCSPTRHGSRVILSLDVPGLILLLEQARARAAREQATTNARILARVG 110
 RESULT 4
 UCN3_MOUSE STANDARD; PRT; 164 AA.
 ID UCN3_MOUSE
 AC Q924A4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Urocortin III precursor (Ucn III).
 GN UCN3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RX MEDLINE=21310014; PubMed=11416224;
 RA Lewis K., Li C., Perrin M.H., Blount A., Kunitake K., Donaldson C.,
 RA Vaughan J., Reyes T.M., Gulyas J., Fischer W., Bilezikjian L.,
 RA Rivier J., Sawchenko P.E., Vale W.W.;
 RT "Identification of urocortin III, an additional member of the
 corticotropin-releasing factor (CRF) family with high affinity for the
 CRF2 receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7570-7575(2001).
 CC -!- FUNCTION: Suppress food intake, delays gastric emptying and
 decreases heat-induced edema. Might represent an endogenous ligand
 for maintaining homeostasis after stress (By similarity).
 CC -!- SUBUNIT: Binds with high affinity to CRF receptors 2-alpha and 2-
 beta.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed in some areas of the brain including
 the hypothalamus, amygdala, and brainstem, but is not evident in
 the cerebellum, pituitary, or cerebral cortex; it is also
 expressed peripherally in small intestine and skin.
 CC -!- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
 factor/urotensin I family.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AF361944; AAK67318.1; -;
 DR MGD; MGI:1932970; Ucn3.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0007189; P:G-protein signaling, adenylate cyclase acti. .; IDA.
 KW Hormone; Amidation; Signal.
 FT SIGNAL 1 23 POTENTIAL.
 FT PROPEP 24 121
 FT CHAIN 123 160 UROCORTIN III.

FT MOD_RES 160 160 AMIDATION (G-161 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 164 AA; 18063 MW; 93A77CB93DA56E5C CRC64;
 Query Match 18.0%; Score 100.5; DB 1; Length 164;
 Best Local Similarity 31.0%; Pred. No. 0.0089;
 Matches 26; Conservative 16; Mismatches 35; Indels 7; Gaps 1;
 QY 36 LETTSSVTSSSTGTTTGPSASWSKASPVLD-----TRVILSLDVPGLILLLE 88
 Db 80 IKRTSGAGNGAGSTRVYQSQAQHGKLVFDRPKSDRGTKFTLSLDVPTNIMKILFN 139
 QY 89 QARYKARNOATNAQILAHVGR 112
 Db 140 IDKAKNLRAKAAANAQLMAQIGK 163
 RESULT 5
 UCN3_HUMAN STANDARD; PRT; 161 AA.
 ID UCN3_HUMAN
 AC Q969E3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Urocortin III precursor (Ucn III) (Stresscopin).
 GN UCN3 OR SPC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RX MEDLINE=21310014; PubMed=11416224;
 RA Lewis K., Li C., Perrin M.H., Blount A., Kunitake K., Donaldson C.,
 RA Vaughan J., Reyes T.M., Gulyas J., Fischer W., Bilezikjian L.,
 RA Rivier J., Sawchenko P.E., Vale W.W.;
 RT "Identification of urocortin III, an additional member of the
 corticotropin-releasing factor (CRF) family with high affinity for the
 CRF2 receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7570-7575(2001).
 CC -!- FUNCTION: Suppress food intake, delays gastric emptying and
 decreases heat-induced edema. Might represent an endogenous ligand
 for maintaining homeostasis after stress.
 CC -!- SUBUNIT: Binds with high affinity to CRF receptors 2-alpha and 2-
 beta.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
 factor/urotensin I family.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AF361943; AAK67317.1; -;
 DR EMBL; AY026949; AAK11729.1; -;
 DR MIM; 605901; -;
 DR MIM; HGNC:17781; UCN3.
 KW Hormone; Amidation; Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT PROPEP 22 118
 FT CHAIN 120 157 UROCORTIN III.
 FT MOD_RES 157 157 AMIDATION (G-158 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 161 AA; 17862 MW; F92B2C8C3087857D CRC64;

```
Query Match 17.8%; Score 99; DB 1; Length 161;
Best Local Similarity 32.5%; Pred. No. 0.012;
Matches 27; Conservative 14; Mismatches 34; Indels 8; Gaps 2;

QY 37 ETTSSVTSSSSGTTTGPSSWSNKSASPILD-----TRVILSDVPIGLRILLEQ 89
DB 79 KTFIS-GARGAGGTRVRYVSQAQPKPDQAKSPHRTKFTLSLDVPTNIMNLLFNI 137
QY 90 ARYZAARNOAATNAQILAHVGR 112
DB 138 AKAKNLRAQAARNAHMAQIGRK 160

RESULT 5
STG2_HUMAN.
ID STG2_HUMAN STANDARD; PRT; 539 AA.
AC Q9NY99;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gamma-2-syntrophin (G2SYN) (Syntrophin 5) (SYN5).
GN SNTG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND INTERACTION WITH DMD; DTNA
RP AND DTNB.
RC TISSUE=Fetal brain, and Neuron;
RX MEDLINE=20283612; PubMed=10747910;
RA Piluso G., Mirabella M., Ricci E., Belsito A., Abbondanza C.,
RA Servidei S., Puca A.A., Tonali P., Puca G.A., Nigro V.;
RT "Gamma1- and gamma2-syntrophins, two novel dystrophin-binding proteins
RT localized in neuronal cells.";
RL J. Biol. Chem. 275:15851-15960(2000).
CC -!- FUNCTION: Adapter protein that binds to and probably organizes the
CC subcellular localization of a variety of proteins. May link
CC various receptors to the actin cytoskeleton and the dystrophin
CC glycoprotein complex (By similarity).
CC -!- SUBUNIT: Interacts with the dystrophin protein DMD and related
CC proteins DTNA and DTNB.
CC -!- SUBCELLULAR LOCATION: Membrane-associated (Probable). In skeletal
CC muscle, it localizes at the cytoplasmic side of the sarcolemmal
CC membrane.
CC -!- TISSUE SPECIFICITY: Widely expressed. Strong expression in brain
CC and testis. In CNS, it is expressed in the perikaryon and proximal
CC portion of the neuronal processes. Strong expression in the
CC hippocampus, neuron-rich dentate granule cells, and pyramidal cell
CC layers. Highly expressed in neurons of the cerebral cortex. Also
CC expressed in the cerebellar cortex, deep cerebellar nuclei,
CC thalamus, and basal ganglia.
CC -!- DOMAIN: The association with dystrophin or related proteins to
CC probably leaves the PDZ domain available to recruit proteins to
CC the membrane (By similarity).
CC -!- SIMILARITY: Belongs to the syntrophin family.
CC -!- SIMILARITY: Contains 1 PDZ/DHR domain.
CC -!- SIMILARITY: Contains 1 PH domain.
CC
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CC
CC -----
CC EMBL; AJ003029; CAB92969.1; -.
CC HSSP; P29476; 1QAV.
CC Genew; HGNC:13741; SNTG2.
CC GO; GO:0016013; C:syntrophin complex; TAS.
CC GO; GO:0007417; P:central nervous system development; TAS.
CC
```

```
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR001849; PH.
DR Pfam; PF00595; PDZ_1.
DR SMART; SM00228; PDZ; 1.
DR SMART; SM00233; PH; 1.
DR PROSITE; PS0106; PDZ; 1.
DR PROSITE; PS0003; PH DOMAIN; FALSE NEG.
KW Actin-binding; Cytoskeleton; Membrane; Multigene family.
FT DOMAIN 73 156
FT DOMAIN 296 421
FT DOMAIN 6 9
FT SEQUENCE 539 AA; 60246 MW; OD3B1E24D2CABF88 CRC64;
QY 26 PTFQLLPQNSLETTPTSSVTSSESS-----GTTTGPSSWSNKSASPILDTRV 72
DB 159 PAFKLPGLGS--PGSSDHSAGSSPLFDSGLHNGNSSTTAPSSPSPIAKDPYKRW 216
QY 73 ILSLDVPIGLRILLEQARYKAARNOAATNA-QILA 107
DB 217 LDTLSVPLSMARI---SRYKAGTEKLRWNAPEVLA 248

RESULT 7
MUCL RAT
ID MUCL RAT STANDARD; PRT; 837 AA.
AC P98089;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Intestinal mucin-like protein (MLP) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RX Xu G., Huan L.-J., Khatri I., Wang D., Bennick A., Fahim R.E.,
RA Forstner G.G., Forstner J.F.;
RT "cDNA for the carboxyl-terminal region of a rat intestinal mucin-like
RT peptide.";
RL J. Biol. Chem. 267:5401-5407(1992).
CC -!- SUBUNIT: Multimeric.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: COATS THE EPITHELIA OF THE INTESTINES.
CC -!- SIMILARITY: Contains 2 VWF domains.
CC -!- SIMILARITY: Contains 1 C-terminal cysteine knot-like (CTCK) domain.
CC
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CC
CC -----
CC EMBL; M81920; -. NOT ANNOTATED_CDS.
CC InterPro; IPR006208; Cys_knot.
CC InterPro; IPR006207; Cys_knot_C.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR002919; TIL_Cysrich.
CC InterPro; IPR001007; VWF_C.
CC InterPro; IPR001846; VWF-D.
CC Pfam; PF00007; Cys_knot; 1.
CC Pfam; PF00093; vwc; 1.
CC Pfam; PF00094; vwd; 1.
CC SMART; SM00041; CT; 1.
CC SMART; SM00214; VWC; 2.
CC
```

SMART; SM00216; VWD; 1.
 DR PROSITE; PS01185; CTCK 1; 1.
 DR PROSITE; PS01225; CTCK 2; 1.
 DR PROSITE; PS00022; EGF 1; UNKNOWN 1.
 DR PROSITE; PS01308; WFEC 1; 2.
 DR PROSITE; PS0184; WFEC 2; 2.
 KW Repeat; Glycoprotein.
 FT NON TER 1
 FT DOMAIN 149 837
 FT DOMAIN 17 70
 FT REPEAT 17 27
 FT REPEAT 28 28
 FT REPEAT 39 50
 FT REPEAT 51 62
 FT REPEAT 63 70
 FT DOMAIN 74 139
 FT DOMAIN 140 517
 FT DOMAIN 472 543
 FT DOMAIN 581 648
 FT DOMAIN 732 817
 FT DISULFID 732 779
 FT DISULFID 746 793
 FT DISULFID 755 809
 FT DISULFID 759 811
 FT DISULFID ? 816
 FT CARBOHYD 91 91
 FT CARBOHYD 164 164
 FT CARBOHYD 278 278
 FT CARBOHYD 289 289
 FT CARBOHYD 344 344
 FT CARBOHYD 410 410
 FT CARBOHYD 444 444
 FT CARBOHYD 515 515
 FT CARBOHYD 538 538
 FT CARBOHYD 612 612
 FT CARBOHYD 627 627
 FT CARBOHYD 695 695
 FT CARBOHYD 727 727
 FT CARBOHYD 749 749
 SQ SEQUENCE 837 AA; 91499 MW; 6335BCDCAC897F35 CRC64;
 Query Match 13.6%; Score 76; DB 1; Length 837;
 Best Local Similarity 37.0%; Pred. No. 12;
 Matches 17; Conservative 11; Mismatches 16; Indels 2; Gaps 1;
 QY 21 PGPIPTFOLLQNSLETTPSSVTSESSGGTTGSPASWSNSKASP 66
 Db 20 PSTPPPTPTTPTSSQTTTPTTPTTSSKSTPTQSS--TSKSTP 63
 RESULT 8
 N214_HUMAN STANDARD; PRT; 2090 AA.
 AC F35658;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Nuclear pore complex protein Nup214 (Nucleoporin Nup214) (214 kDa
 DE nucleoporin) (CAN protein).
 GN NUP214 OR CAN OR CAN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Testis;
 RX MEDLINE=92195315; PubMed=1549122;
 RA Von Lindern M., Fornierod M., Van Baal S., Jaegle M., De Wit T.,
 RA Buijs A., Grosveld G.;

RT "The translocation (6;9), associated with a specific subtype of acute
 RT myeloid leukemia, results in the fusion of two genes, dek and can,
 RT and the expression of a chimeric, leukemia-specific dek-can mRNA.";
 RL Mol. Cell. Biol. 12:1687-1697(1992).
 RP [2].
 RN CHARACTERIZATION.
 RX MEDLINE=94151361; PubMed=8108440;
 RA Kraemer D., Wozniak R.W., Blobel G., Radu A.;
 RT "The human CAN protein, a putative oncogene product associated with
 RT myeloid leukemogenesis, is a nuclear pore complex protein that faces
 RT the cytoplasm.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:1519-1523(1994).
 CC -!- FUNCTION: May serve as a docking site in the receptor-mediated
 CC import of substrates across the nuclear pore complex.
 CC -!- SUBUNIT: Homodimer. Interacts with DDX19 and NUP88.
 CC -!- SUBCELLULAR LOCATION: Nuclear pore complex. Cytoplasmic filaments.
 CC -!- TISSUE SPECIFICITY: Expressed in thymus, spleen, bone marrow,
 CC kidney, brain and testis, but hardly in all other tissues or in
 CC whole embryos during development.
 CC -!- DOMAIN: Contains F-G repeats.
 CC -!- PTM: Probably glycosylated as it reacts with wheat germ agglutinin
 CC (WGA).
 CC -!- DISEASE: Implicated in a subset of acute myeloid leukemia (acute
 CC nonlymphocytic leukemia) (AML) carrying a chromosomal
 CC translocation t(6;9)(p23;q34) that results in the formation of a
 CC DEK-CAN fusion gene.
 CC -!- DISEASE: Involved in some cases of acute undifferentiated leukemia
 CC (AUL) through a chromosomal translocation t(6;9)(q21;q34.1) that
 CC involves NUP214/CAN and SET.
 CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobiogen.fr/services/chronocancer/genes/CAN.html".
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X64228; CAA45535.1; -;
 CC FIR; S26058; S26058.
 CC Genew; HGNC:8064; NUP214.
 CC MIM; 114350; -;
 CC GO; GO:0005643; C:nuclear pore; TAS.
 CC GO; GO:0005215; F:transporter activity; TAS.
 CC InterPro; IPR004325; Nucleoporin_FG.
 CC Pfam; PF03093; Nucleoporin_FG; 22.
 CC SMART; SM00320; WD40; 2.
 CC KW Nuclear protein; Transport; Proto-oncogene; Chromosomal translocation;
 KW Repeat; Glycoprotein.
 FT DOMAIN 461 2076
 FT DOMAIN 1409 2084
 FT DOMAIN 1427 2085
 FT DOMAIN 1213 2090
 FT DOMAIN 740 768
 FT DOMAIN 861 882
 FT SITE 812 813
 FT SITE BREAKPOINT.
 SQ SEQUENCE 2090 AA; 213766 MW; 6DBE767FDD857F8F CRC64;
 Query Match 13.6%; Score 75.5; DB 1; Length 2090;
 Best Local Similarity 43.1%; Pred. No. 36;
 Matches 22; Conservative 4; Mismatches 20; Indels 5; Gaps 2;
 QY 21 PGPIPTFOLLQNSLETTPSSVTSESSGGTTGSPASWSNSKASP 66
 Db 463 PAAPATPTSLPAGGAPTVPFGSSSLKSSATVTGEPSPSSGSDSKAAP 513
 RESULT 9
 CRF_HUMAN STANDARD; PRT; 196 AA.
 ID CRF_HUMAN

P06850;
01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Corticotropin precursor (Corticotropin-releasing factor) (CRF)
(Corticotropin releasing hormone).
CRH.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
SEQUENCE FROM N.A.
MEDLINE=84057755; PubMed=6605851;
Shibahara S., Morimoto Y., Furutani Y., Notake M., Takahashi H.,
Shimizu S., Horikawa S., Numa S.,
"Isolation and sequence analysis of the human corticotropin-releasing
factor precursor gene."
EMBO J. 2:775-779(1993).
[2]
SEQUENCE FROM N.A.
MEDLINE=89137721; PubMed=2783917;
Robinson B.G., D'Angio L.A. Jr., Pasieka K.B., Maizoub J.A.;
"Proprocorticotropin releasing hormone: cDNA sequence and in vitro
processing."
Mol. Cell. Endocrinol. 61:175-180(1989).
[3]
SEQUENCE FROM N.A.
TISSUE=Brain;
MEDLINE=2238257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smaluk D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
STRUCTURE BY NMR OF 154-194.
MEDLINE=9323434; PubMed=8386360;
Romier C., Bernassau J.-M., Cambillau C., Darbon H.;
"Solution structure of human corticotropin releasing factor by 1H NMR
and distance geometry with restrained molecular dynamics."
Protein Eng. 6:149-156(1993).
-1- FUNCTION: This hormone from hypothalamus regulates the release of
corticotropin from pituitary gland.
-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
factor/urotensin I family.

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EMBL; V00571; CAA23834.1; --
EMBL; BC002599; AA02599.1; --

DR EMBL; BC011031; AAH1031.1; --
DR PIR; A30327; A30327.
DR Genew; HGNC:2355; CRH.
DR MIM; 122560; --
DR GO; GO:0005625; C-soluble fraction; TAS.
DR GO; GO:0005184; F-neuropeptide hormone activity; TAS.
DR GO; GO:0007611; P-learning and/or memory; TAS.
DR GO; GO:0007567; P-parturition; TAS.
DR GO; GO:0007565; P-pregnancy; TAS.
DR GO; GO:0007165; P-signal transduction; TAS.
DR GO; GO:0007268; P-synaptic transmission; TAS.
DR InterPro; IPR000187; corticoliberin.
DR InterPro; IPR003620; Urocortin_CRF.
DR Pfam; PF00473; CRF; 1.
DR PRINTS; PRO1612; CRFFAMILY.
DR ProDom; PD005970; Urocortin_CRF; 1.
DR SMART; SM00039; CRF; 1.
DR PROSITE; PS00511; CRF; 1.
KW Hormone; Amidation; Hypothalamus; Cleavage on pair of basic residues;
KW Signal.
KW SIGNAL 1 24 PROBABLE.
FT PROPEP 25 153 CORTICOLIBERIN.
FT PEPTIDE 154 194
FT MOD RES 194 194
SQ SEQUENCE 196 AA; 21422 MW; 0CCDF05BE364E92 CRC64;
Query Match 13.4%; Score 74.5; DB 1; Length 196;
Best Local Similarity 26.8%; Pred. No. 3.3;
Matches 22; Conservative 19; Mismatches 36; Indels 5; Gaps 2;
QY 30 LLPQNSLETTPTSPVTSSESGTTTGPSAGSNWSKASPYLDTRVILSDVPIGLRLLEQ 89
DQ 120 LLPRLSLD-SPAALAEAGARNALCGHQEAPERRRS-----EPPISLDLTFHLLREVLEM 174
QY 90 ARYKAARNAQATNAQILAHVGR 111
DQ 175 ARAEQLAQAQSHNRKLMETIGK 196
RESULT 10
VV SV5
ID VV SV5 STANDARD; PRT; 222 AA.
AC P11207;
DT 01-JUL-1999 (Rel. 11, Created)
DT 01-JUL-1999 (Rel. 11, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Nonstructural protein V.
GN P/V
OS Simian virus 5 (strain W3) (SV5).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OC NCBI_TaxID=11208;
RN [1]
RP SEQUENCE FROM N.A., AND RNA EDITING.
EX MEDLINE=8311091; PubMed=3044614;
RA Thomas S.M., Lamb R.A., Paterson R.G.;
RT "Two mRNAs that differ by two nontemplated nucleotides encode the
RT amino terminal proteins P and V of the paramyxovirus SV5."
RL Cell 54:891-902(1988).
CC -1- RNA EDITING: Modified positions=164; Note-Partially edited. RNA
CC editing at this position consists of an insertion of two guanine
CC nucleotides. The sequence displayed here is the V protein, derived
CC from the unedited RNA. The edited RNA gives rise to the P protein
CC (AC P11208).
CC -1- SIMILARITY: TO THE V PROTEIN OF OTHER PARAMYXOVIRUSES.

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EMBL; V00571; CAA23834.1; --
EMBL; BC002599; AA02599.1; --

CC DR EMBL; J03142; AAA47882.1; --
CC DR EMBL; AF052755; AAC95512.1; --
CC DR PIR; A31594; MNZSP.
CC DR InterPro; IPR004897; Paramyx_P_V.
CC DR Pfam; PF03210; Paramyx_P_V; 1.
CC DR Nonstructural protein; RNA editing.
CC FT DOMAIN 190 218 CYS-RICH
CC SQ SEQUENCE 222 AA; 23935 MW; 13D2F1627D15AFA3 CRC64;

Query Match 12.8%; Score 71.5; DB 1; Length 222;
Best Local Similarity 32.3%; Pred. No. 7.3;
Matches 31; Conservative 9; Mismatches 29; Indels 27; Gaps 5;

Qy 20 VPGTPIPTFOLLPPNSLETTPTSSVTSSSGTTTGPASMSNSKASPY-----LDTRVLS 75
Db 93 VPQKPIPN-----PLGLGDSPTSTQTVLDLSGKTL-PEGSGYGVKLAKFGKENVLTFRI-- 145
Qy 76 LDVPIGLLRILLEQARYKAARNOAATNAQILAHVGR 111
Db 146 -----EEPR-----ENPIATSSPIDFKRGR 165

RESULT 11
GCM1 MOUSE
ID GCM1_MOUSE STANDARD; PRT; 436 AA.
AC P70348; O09103;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Chorion-specific transcription factor GCMa (Glial cells missing homolog 1) (GCM motif protein 1) (mGCMa) (mGCM1).
GN GCM1 OR GCMa.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
TX TISSUE=Placenta;
RX MEDLINE=96409308; PubMed=8814290;
RA Altschuller Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Frohman M.A.;
RT "Gcm1, a mammalian homolog of Drosophila glial cells missing."
RL FEBS Lett. 393:201-204(1996).
[2]
SEQUENCE FROM N.A.
TX TISSUE=Placenta;
RX MEDLINE=97121489; PubMed=8962155;
RA Akiyama Y., Hosoya T., Poole A.M., Hotta Y.;
RT "The gcm-motif: a novel DNA binding motif conserved in Drosophila and mammals."
RL Proc. Natl. Acad. Sci. U.S.A. 93:14912-14916(1996).
CC -!- FUNCTION: Transcription factor that is necessary for placental development (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- TISSUE SPECIFICITY: Placenta specific.
CC -!- SIMILARITY: Contains 1 GCM domain.

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CC -----
CC EMBL; U59876; AAC52822.1; --
CC DR EMBL; D88612; BAAL3650.1; --
CC PIR; S74257; S74257.
CC DR TRANSPAC; T02307; --
CC MGD; MGI:108045; Gcm1.
CC GO; GO:0003677; F:DNA binding; IDA.

DR GO; GO:0008270; F:zinc ion binding; IDA.
DR InterPro; IPR003902; GCM_motif.
DR Pfam; PF03615; GCM; 1.
DR PROSITE; PS0807; GCM; 1.
KW Transcription regulation; DNA-binding; Nuclear protein;
KW Developmental protein.
FT DOMAIN 14 169 GCM.
FT CONFLICT 211 211 G -> S (IN REF. 2).
FT CONFLICT 230 230 N -> K (IN REF. 2).
FT CONFLICT 241 241 S -> N (IN REF. 2).
FT CONFLICT 413 413 D -> E (IN REF. 2).
SQ SEQUENCE 436 AA; 49589 MW; 99F4E441800582DB CRC64;

Query Match 12.8%; Score 71.5; DB 1; Length 436;
Best Local Similarity 35.3%; Pred. No. 15;
Matches 24; Conservative 6; Mismatches 31; Indels 7; Gaps 4;

Qy 18 LFVGTPTPT-----FQLLP-QNSLETTPTSSVTSSSGTTTGPASMSNSKASPYLD-TR 71
Db 311 IYYPALPLFVASWPYDYFPFNSLHLPQQVPSEPPA-AQPCCHLWNSPGEPIEKVS 369
Qy 72 VILSLDVP 79
Db 370 VDLSSVVP 377

RESULT 12
AB31 ARATH
ID AB31 ARATH STANDARD; PRT; 519 AA.
AC Q9FYI3;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Inner membrane ALBINO3-like protein 1, chloroplast precursor (Atb4).
GN ALB31 OR ATIG24490 OR F2109.16.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
[1]
SEQUENCE FROM N.A.
TX STRAIN=cv. Columbia;
RX MEDLINE=20106719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., Dewar K.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dwyer K.,
RA Dunn P., Egu P., Feildlyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Millescher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Xu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis thaliana."
RL Nature 408:816-820(2000).
CC -!- FUNCTION: Probably required for the insertion of integral membrane proteins into the chloroplast thylakoid membrane (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast thylakoid membrane (Potential).
CC -!- SIMILARITY: Belongs to the OXA1/OXA family.

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EMBL: AC000103; AAF97961.1; --

PIR: H86378; H86378; 60kDa innermem.

InterPro: IPR001708; 60kDa IMP; 1.

Pfam: PF02096; 60kDa IMP; 1.

Chloroplast; Membrane; Inner membrane; Transit peptide; Transmembrane.

TRANSIT 1 519 CHLOROPLAST (POTENTIAL).

CHAIN 1 519 INNER MEMBRANE ALBINOS-LIKE PROTEIN 1.

TRANSMEM 115 135 POTENTIAL.

TRANSMEM 147 167 POTENTIAL.

TRANSMEM 204 224 POTENTIAL.

TRANSMEM 283 303 POTENTIAL.

TRANSMEM 322 342 POTENTIAL.

SEQUENCE 519 AA; 57507 MW; A4CE0A5EBF2CB769 CRC64;

Query Match 12.8%; Score 71.5; DB 1; Length 519;

Best Local Similarity 31.3%; Pred. No. 19;

Matches 26; Conservative 11; Mismatches 31; Indels 15; Gaps 3;

QY 41 SSVTSSESSGTTTPSAS--WSNKAQPYLDT-----RVILSLDVPGLRL 86

DB 76 SSETFESVAGTTTKTQSDNWFSGIAN-YMETILKVLKGLSTVHVPSYGFALLTLVL 134

QY 87 LEQARYKAARQAATNAQILAHV 109

DB 135 VQAATPPTKKQVFMISFLVHV 157

RESULT 13

WMT1 RAT STANDARD; PRT; 521 AA.

AC Q01818;

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Chromaffin granule amine transporter (Vesicular amine transporter 1)

DE (VAT1) (Solute carrier family 18 member 1).

GN SLC18A1 OR VMAT1 OR CGAT.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP MEDLINE=92370677; PubMed=1505023;

RA Liu Y., Peter D., Rochani A., Schuldiner S., Prive G.G.,

RA Eisenberg D., Brecha N., Edwards R.H.;

RT "A cDNA that suppresses MPP+ toxicity encodes a vesicular amine transporter."

RL Cell 70:539-551(1992).

CC -!- FUNCTION: Involved in the vesicular transport of biogenic amines.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Vesicular membrane.

CC -!- TISSUE SPECIFICITY: Adrenal gland.

CC -!- SIMILARITY: Belongs to the major facilitator (MFS) superfamily. Vesicular transporter family.

CC

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CC

CC EMBL: M97380; AAA40921.1; --

PIR: A43319; A43319.

DR InterPro: IPR007114; MFS.

DR InterPro: IPR005828; Sub transporter.

Pfam: PF00083; sugar_tr; 1.

DR PROSITE; PS0850; MFS; 1.

KW Transport; Transmembrane; Glycoprotein; Neurotransmitter transport.

FT DOMAIN 1 21 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 22 42 POTENTIAL.

FT DOMAIN 43 135 VESICULAR LUMEN (POTENTIAL).

FT TRANSMEM 136 155 POTENTIAL.

FT DOMAIN 156 164 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 165 185 POTENTIAL.

FT DOMAIN 186 194 VESICULAR LUMEN (POTENTIAL).

FT TRANSMEM 195 215 POTENTIAL.

FT DOMAIN 216 224 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 225 247 POTENTIAL.

FT DOMAIN 248 253 VESICULAR LUMEN (POTENTIAL).

FT TRANSMEM 254 276 POTENTIAL.

FT DOMAIN 277 296 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 297 316 POTENTIAL.

FT DOMAIN 317 332 VESICULAR LUMEN (POTENTIAL).

FT TRANSMEM 333 357 POTENTIAL.

FT DOMAIN 358 382 POTENTIAL.

FT TRANSMEM 383 394 VESICULAR LUMEN (POTENTIAL).

FT DOMAIN 394 415 POTENTIAL.

FT TRANSMEM 416 419 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 420 440 VESICULAR LUMEN (POTENTIAL).

FT TRANSMEM 441 445 POTENTIAL.

FT DOMAIN 446 467 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 468 521 POTENTIAL.

FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 521 AA; 55935 MW; DCD0D0A0F0EC15D4 CRC64;

Query Match 12.8%; Score 71.5; DB 1; Length 521;

Best Local Similarity 33.3%; Pred. No. 19;

Matches 22; Conservative 8; Mismatches 25; Indels 11; Gaps 2;

QY 6 LVVVFVLLMLDRILFVPGTPI-PTFQLLPQNSLETTPSVTSSESSGTTTPGSASWSNSKA 64

DB 25 VVVFVALLDMLLTVVVPIVFLY-----ATEFKDSNLSLRGSPVSSQALT 74

QY 65 SPYLDT 70

DB 75 SPAFST 80

RESULT 14

AMTH YEAST STANDARD; PRT; 1367 AA.

AC P08640; P08068;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Glucosylase S1/S2 precursor (EC 3.2.1.3) (Glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucosylase).

DE STAI OR STAI2 OR MAL5 OR YIR019C.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes.

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=S288c / AB972;

RE MEDLINE=97313266; PubMed=9169870;

RA Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D.,

RA Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,

RA Harris D.B., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,

RA Moulé S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,

RA Skelton J., Smith V., Walsh S., Whitehead M., Barrell B.G.;

RL "The nucleotide sequence of Saccharomyces cerevisiae chromosome IX.;"

RL Nature 387:84-87(1997).

RN [2]

RP SEQUENCE OF 1-242 AND 762-1331 FROM N.A.

RX MEDLINE=87194600; PubMed=3106330;

RA Yamashita I., Nakamura M., Fukui S.;
 RT "Gene fusion is a possible mechanism underlying the evolution of
 RT STAI.";
 RT J. Bacteriol. 169:2142-2149 (1987).
 RN [3]
 RN SEQUENCE OF 1-31 FROM N.A.
 RC STRAIN=SPX101-1C;
 RX MEDLINE=89031230; PubMed=3141213;
 RX Pardo J.M., Ianez E., Zalacain M., Claros M.G., Jimenez A.;
 RT "Similar short elements in the 5' regions of the STA2 and SGA genes
 RT from Saccharomyces cerevisiae.";
 RL FEBS Lett. 239:179-184 (1988).
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-
 CC glucose residues successively from non-reducing ends of the chains
 CC with release of beta-D-glucose.
 CC -!- SIMILARITY: TO S.POMBE SPBC215.13.
 CC -!- SIMILARITY: SOME, TO S.POMBE SFCC285.13C.
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 CC
 CC EMBL; Z38061; CAA86176.1; -
 CC EMBL; M16164; AAA35014.1; -
 CC EMBL; M16165; AAA35015.1; -
 CC EMBL; X13857; CAA32069.1; -
 CC PIR; S48478; S48478.
 CC Germonline; 139731; -
 CC SGD; S0001458; MUC1.
 CC GO; GO:0005886; C:plasma membrane; IDA.
 CC GO; GO:0030447; P:filamentous growth; IDA.
 CC GO; GO:0007125; P:invasive growth; IMP.
 CC GO; GO:0007124; P:pseudophal growth; IMP.
 CC Hydrolase; Glycosidase; Polysaccharide degradation; Glycoprotein;
 CC Signal; Multigene family.
 CC SIGNAL 1 21
 CC CHAIN 22 1367
 CC DOMAIN 210 1367
 CC CARBOHYD 817 817
 CC CARBOHYD 874 874
 CC SEQUENCE 1367 AA; 136110 MW; 91C0E2DBD61AA9D CRC64;
 Query Match 12.7%; Score 71; DB 1; Length 1367;
 Best Local Similarity 38.6%; Pred. No. 61;
 Matches 17; Conservative 6; Mismatches 9; Indels 12; Gaps 1;
 Qy 23 TPITPQLPONSLETTPTSSVTSSSGTTTGPASWSNKSASP 66
 Db 312 TPVP-----TPSSSTSSSAPVPTPSSSTSSAP 343
 RESULT 15
 RPP SVS
 ID RPP SVS STANDARD; PRT; 392 AA.
 AC P11208
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE RNA polymerase alpha subunit (EC 2.7.7.48) (P protein).
 GN P/V.
 OS Simian virus 5 (strain W3) (SV5).
 OC Viruses; sRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
 OX NCBI_TaxID=11208;
 RN [1]
 RN SEQUENCE FROM N.A., AND RNA EDITING.
 RP MEDLINE=88311091; PubMed=304614;
 RA Thomas S.M., Lamb R.A., Paterson R.G.;
 RA "Two mRNAs that differ by two nontemplated nucleotides encode the

RT amino coterminal proteins P and V of the paramyxovirus SV5.";
 RL Cell 54:891-902 (1988).
 CC -!- FUNCTION: Essential component of the RNA polymerase and the
 CC nascent chain assembly complex. Also required during RNA
 CC synthesis.
 CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC [RNA] (N).
 CC -!- RNA EDITING: Modified positions=164; Note-Partially edited. RNA
 CC editing at this position consists of an insertion of two guanine
 CC nucleotides. The sequence displayed here is the P protein, derived
 CC from the edited RNA. The unedited RNA version gives rise to the V
 CC protein (AC P11207).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; J03142; -; NOT ANNOTATED_CDS.
 CC EMBL; AF052755; AAC95513.1; -
 CC PIR; B31594; RMNZSP.
 CC InterPro: IPR004897; Paramyx_P_V_1
 CC Pfam: PF03210; Paramyx_P_V_1
 CC Transfrase; RNA-directed RNA polymerase; Nucleocapsid;
 CC Phosphorylation; RNA editing.
 CC SEQUENCE 392 AA; 42106 MW; A95D21FD125E8559 CRC64;
 Query Match 12.7%; Score 70.5; DB 1; Length 392;
 Best Local Similarity 39.7%; Pred. No. 17;
 Matches 23; Conservative 6; Mismatches 20; Indels 9; Gaps 3;
 Qy 20 VPGTPTPTFOLLPONSLETTPTSSVTSSSGTTTGPASWSNKSAPY---LQTRVI 73
 Db 93 VEGKPIPN---PLIGLSTPTSTQVLDLSGKTL-PSGSYKGVKLAKFKENLMTRFI 145
 Search completed: April 20, 2004, 18:55:21
 Job time : 20.9333 secs

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OM protein - protein search, using sw model

Run on: April 20, 2004, 18:52:07 ; Search time 20.16 Seconds
(without alignments)

534.397 Million cell updates/sec

Title: US-09-919-473-10

Perfect score: 557

Sequence: 1 MTRWLVVFWLMLDRILEV.....KAARNOATNAQILAHVGR 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	14.2	338	T39159	hypothetical prote
2	77.5	13.9	889	AB0790	probable two-compo
3	76	13.6	837	A42112	mucin-like peptide
4	75.5	13.6	2090	S26088	probable transform
5	74.5	13.4	196	A30327	corticoliberin pre
6	74	13.3	2578	A56922	transcription fact
7	73.5	13.2	164	I53641	mucin 5AC - human
8	73	13.1	125	D72475	hypothetical prote
9	73	13.1	802	G87578	TonB-dependent rec
10	72.5	13.0	486	E55886	dopamine receptor
11	72.5	13.0	526	T14875	hypothetical prote
12	72.5	13.0	3283	AC1018	large repetitive p
13	72	12.9	431	T38260	hypothetical prote
14	71.5	12.8	222	MNN28P	nonstructural prot
15	71.5	12.8	276	T29689	hypothetical prote
16	71.5	12.8	436	S74257	glial cells missin
17	71.5	12.8	519	H86378	protein P21J9.16 [
18	71.5	12.8	521	A43319	chromaffin granule
19	71.5	12.8	2529	A56923	transcription fact
20	71	12.7	476	T23728	hypothetical prote
21	71	12.7	1367	A48478	glucan 1,4-alpha-g
22	71	12.7	1796	AC1895	serine/threonine k
23	70.5	12.7	392	RN23SP	polymerase-associa
24	70.5	12.7	1036	B83466	probable RND efflu
25	70.5	12.7	4377	A55575	ankyrin 3, long sp
26	70	12.6	247	H71565	hypothetical prote
27	70	12.6	292	I51171	transcription fact
28	70	12.6	402	G90254	conserved hypothet
29	70	12.6	500	JC2231	prostaglandin-I sy

30	69.5	12.5	187	1	RHRTCE	corticoliberin pre
31	69.5	12.5	322	2	F84616	probable BHLH tran
32	69.5	12.5	636	2	S63131	probable membrane
33	69.5	12.5	1324	2	S52863	DNA-binding protei
34	69	12.4	549	2	S32987	hypothetical prote
35	69	12.4	682	2	T47473	receptor-like prot
36	69	12.4	808	2	T23129	hypothetical prote
37	69	12.4	1151	2	T18535	high molecular mas
38	68.5	12.3	532	2	T38658	vesicular acetylch
39	68	12.2	122	2	S60262	corticotensin - ra
40	68	12.2	145	1	UOCA1	urotensin I precur
41	68	12.2	162	2	A31343	corticoliberin 1 p
42	68	12.2	254	2	D88560	protein F58A4.1 [i
43	68	12.2	303	2	S40973	hypothetical prote
44	68	12.2	469	1	P2WLPR	L2 protein - human
45	68	12.2	580	2	T37664	hypothetical prote

ALIGNMENTS

RESULT 1

T39159
hypothetical protein SPAC8E11.05c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
C:Accession: T39159
R:McLean, J.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, February 1998
A:Reference number: Z21831
A:Accession: T39159
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-338 <NCU>
A:Cross-references: EMBL:AL021817; PIDN:CAA17026.1; GSPDB:GN00066; SPDB:SPAC8E11.05c
A:Experimental source: strain 972h-; cosmid c8E11
C:Genetics:
A:Gene: SPDB:SPAC8E11.05c
A:Map position: 1
C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC8E11.05c

Query Match 14.2%; Score 79; DB 2; Length 338;
Best Local Similarity 27.7%; Pred. No. 2.6;
Matches 28; Conservative 9; Mismatches 28; Indels 36; Gaps 3;

QY 8 VFVWLMRLDRILFVPGTPTFTFOLLPONSLETTPTSPSVTSSSGTTPGSAWSNSKASPY 67

Db 202 IFIVTM-----GLPVDLELLP-----TFSTQGSFNSRTIELSLSSVILPKSEDEPY 247

QY 68 LPTRVILSDVPFGLRLILLEQARYKAARNOATNAQILAH 108

Db 248 LD-----YSAARRLCSINKDALTH 266

RESULT 2

AB0790
probable two-component system sensor kinase STY2494 [imported] - Salmonella enterica sub:
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 03-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AB0790
R:Farkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovi
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AB0790
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-889 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD07500.1; PID:gi6503495; GSPDB:GN00176

C:Genetics:
A:Gene: STY2494

Query Match 13.9%; Score 77.5; DB 2; Length 889;
Best Local Similarity 26.4%; Pred. No. 12;
Matches 33; Conservative 18; Mismatches 39; Indels 35; Gaps 5;

QY 18 LPVPTPTPTTOLLP-----QNSLETPPSVTSE-----SSSGTTTGPSASWSNS 62
DB 238 LPPGWNPLDSFEDATQTTGSRSEKAPDVTISFNGSKIEISSALNSTGMLWQVP 297
QY 63 KASPYLDT--RVILSDVPGLRILL-----EQARYKAARQ-----AATN 102
DB 298 FGTLLDITLQNTLLPULLNIGLLALFGYATFRHQGRSTESTSGNAANNELRVLRAIN 357
QY 103 AQILA 107
DB 358 EIVS 362

RESULT 3
A42112
mucin-like peptide MLP 2677 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 10-Oct-1997
C:Accession: A42112
R:Yu, G.; Huan, L.J.; Khatri, I.A.; Wang, D.; Bennick, A.; Fahim, R.E.; Forstner, G.G.;
J. Biol. Chem. 267, 5401-5407, 1992
A:Title: cDNA for the carboxyl-terminal region of a rat intestinal mucin-like peptide.
A:Reference number: A42112; MUID:92184794; PMID:1371999
A:Accession: A42112
A>Status: preliminary
A:Molecule type: nucleic acid; protein
A:Residues: 1-837 <XU1>
A:Experimental source: intestine
A>Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIP:87420)
C:Superfamily: von Willebrand factor type C repeat homology
F:582-650/Domain: von Willebrand factor type C repeat homology <WVC>

Query Match 13.6%; Score 76; DB 2; Length 837;
Best Local Similarity 37.0%; Pred. No. 16;
Matches 17; Conservative 11; Mismatches 16; Indels 2; Gaps 1;

QY 21 PGTPIPTFOLLQNSLETPPSVTSESSSGTTGPSASWSNSKASP 66
DB 20 PSTPPPTPTTPTTSOTTPTTPTTSKSTPTFQS--TSSKSTP 63

RESULT 4
S26058
probable transforming protein (can) - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C:Accession: S26058
R:van Lindern, M.; Fornierod, M.; van Baal, S.; Jaegle, M.; de Wit, T.; Buijs, A.; Grosveld
Mol. Cell. Biol. 12, 1687-1697, 1992
A:Title: The translocation (6;9), associated with a specific subtype of acute myeloid le
k-can mRNA.
A:Reference number: S26058; MUID:92195315; PMID:1549122
A:Accession: S26058
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2090 <VON>
A:Cross-references: EMBL:X64228; NID:g29652; PIDN:CAA45535.1; PID:g29653

Query Match 13.6%; Score 75.5; DB 2; Length 2090;
Best Local Similarity 43.1%; Pred. No. 52;
Matches 22; Conservative 4; Mismatches 20; Indels 5; Gaps 2;

QY 21 PGTPIPTFOLLQNSLETPPSVTSESSSGTTGPSASWSNSKASP 66
DB 463 PAAPATFSLPAGGAPTTFVFGSSSLKSSATVTGPPPSYSSGSDSKAAP 513

RESULT 5

A30327
corticotropin precursor - human
N:Alternate names: corticotropin-releasing factor
N:Contains: corticotropin
C:Species: Homo sapiens (man)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Jul-1999
C:Accession: A30327; A60860; I38106
R:Robinson, B.G.; D'Angio Jr., L.A.; Pasieka, K.B.; Majzoub, J.A.
Mol. Cell. Endocrinol. 61, 175-180, 1989
A:Title: Preprocorticotropin releasing hormone: cDNA sequence and in vitro processing.
A:Reference number: A30327; MUID:89137721; PMID:2783917
A:Accession: A30327
A>Status: not compared with conceptual translation
A:Molecule type: mRNA

A:Residues: 1-196 <ROB>
R:Sasaki, A.; Tempst, P.; Liotta, A.S.; Margioris, A.N.; Hood, L.E.; Kent, S.B.H.; Sato, J. Clin. Endocrinol. Metab. 67, 768-773, 1988
A:Title: Isolation and characterization of a corticotropin-releasing hormone-like peptide
A:Reference number: A60860; MUID:88331316; PMID:3262120
A:Accession: A60860
A:Molecule type: protein
A:Residues: 134-168, X, 170-186 <SAS>
R:Shibahara, S.; Morimoto, Y.; Furutani, Y.; Notake, M.; Takahashi, H.; Shimizu, S.; Horii
EMBO J. 2, 775-779, 1983
A:Title: Isolation and sequence analysis of the human corticotropin-releasing factor precursor
A:Reference number: I38106; MUID:84057755; PMID:6605951
A:Accession: I38106
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-196 <RES>
A:Cross-references: EMBL:V00571; NID:g35355; PIDN:CAA23834.1; PID:g35356
C:Genetics:

A:Gene: GDB:CRH
A:Cross-references: GDB:119804; OMIM:122560
A:Map position: qg13-8q13
C:Superfamily: corticotropin-endorphin; diuretic hormone homology
C:Keywords: amidated carboxyl end; hormone; hypothalamus; placenta
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-196/Product: corticotropin #status predicted <MAT>
F:154-194/Product: corticotropin #status predicted <CLN>
F:154-193/Domain: diuretic hormone homology <DBH>
F:194/Modified site: amidated carboxyl end (Ile) (amide in mature form from following gly

Query Match 13.4%; Score 74.5; DB 2; Length 196;
Best Local Similarity 26.8%; Pred. No. 3.9;
Matches 22; Conservative 19; Mismatches 36; Indels 5; Gaps 2;

QY 30 LLPONSLETPPSVTSESSSGTTGPSASWSNSKASPYLDTRVILSDVPGLRILLEQ 89
DB 120 LLPRSUD-SFALAERGAALGGHQAEPERRS-----EPPISLDLTFLLRVLEM 174

QY 90 ARYKAARNQATNAQILAHYGR 111
DB 175 ARAEQLAQAQAHNRKLMETICK 196

RESULT 6

A56922

transcription factor shn - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 17-Mar-1999

C:Accession: A56922

R:Arora, K.; Dai, H.; Kazuko, S.G.; Jamal, J.; O'Connor, M.B.; Letsou, A.; Warrior, R.

Cell 81, 781-790, 1995

A:Title: The Drosophila schnurri gene acts in the Dpp/TGFbeta signaling pathway and encodes

A:Reference number: A56922; MUID:95292345; PMID:7774017

A:Accession: A56922

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar

A:Molecule type: mRNA

A:Residues: 1-2578 <ARO>

Qy

hypothetical protein - Salmonella typhimurium
C/Species: Salmonella typhimurium
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
A/Accession: T14875
R/Wong, K.K.; McClelland, M.; Stillwell, L.C.; Sisk, E.C.; Thurston, S.J.; Saffer, J.D.
Infect. Immun. 66, 3365-3371, 1998
A/Title: Identification and sequence analysis of a 27-kilobase chromosomal fragment containing typhimurium LT2.
A/Reference number: Z18249; MUID:98298059; PMID:9632606
A/Accession: T14875
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-526 <WON>
A/Cross-references: EMBL:AF060869; NID:g3323584; PID:g3323592; PIDN:AAC26644.1
C/Genetics:
A/Gene: spi4_F
A/Map position: 92 min

Query Match 13.0%; Score 72.5; DB 2; Length 526;
Best Local Similarity 29.2%; Pred. No. 20;
Matches 21; Conservative 14; Mismatches 22; Indels 15; Gaps 3;
QY 10 VVLMRLILFVPGTPIPTFOLLPONSLETPSSVTSSSGTTGTPS---ASWSNSKASP 66
Db 162 LVITIDSV-----TDKPTFELSP-----SSVSGHGKLTPTLTPTSVIGTAEENAKVDI 209

QY 67 YLDTREVILSLDV 78
Db 210 YVDNKLVASVDV 221

RESULT 12
AC1018
large repetitive protein [imported] - Salmonella enterica subsp. enterica serovar Typhi
C/Species: Salmonella enterica subsp. enterica serovar Typhi
A/Note: this species has also been called Salmonella typhi
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C/Accession: AC1018
R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Aitfield: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi
A/Reference number: AB0502; MUID:21534947; PMID:11677608
A/Accession: AC1018
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-3283 <PAR>
A/Cross-references: GB:AL513382; PIDN:CAD09244.1; PID:G16505248; GSPDB:GN00176
C/Genetics:
A/Gene: STY4458

Query Match 13.0%; Score 72.5; DB 2; Length 3283;
Best Local Similarity 29.2%; Pred. No. 1.8e+02;
Matches 21; Conservative 14; Mismatches 22; Indels 15; Gaps 3;
QY 10 VVLMRLILFVPGTPIPTFOLLPONSLETPSSVTSSSGTTGTPS---ASWSNSKASP 66
Db 326 LVITIDSV-----TDKPTFELSP-----SSVSGHGKLTPTLTPTSVIGTAEENAKVDI 373

QY 67 YLDTREVILSLDV 78
Db 374 YVDNKLVASVDV 385

RESULT 13
T38260
hypothetical protein SPAC23C4.05c - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C/Accession: T38260
R/Harris, D.; Squares, R.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

submitted to the EMBL Data Library, September 1997
A/Reference number: Z21782
A/Accession: T38260
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-431 <HAR>
A/Cross-references: EMBL:Z99753; PIDN:CAB16876.1; GSPDB:GN00066; SPDB:SPAC23C4.05c
A/Experimental source: strain 972h; cosmid c23C4
C/Genetics:
A/Gene: SPDB:SPAC23C4.05c
A/Map position: 1
A/Introns: 23/1

Query Match 12.9%; Score 72; DB 2; Length 431;
Best Local Similarity 23.6%; Pred. No. 18;
Matches 21; Conservative 16; Mismatches 38; Indels 14; Gaps 2;
QY 32 PONSLETPSSVTSSSGTTGTPSASWSNSKASPYLDTRVILSLDV-----P 79
Db 43 PPTTKYVQRTVYAGREKGIKGGPADSWPQKLDLDFLQNHGVKSLDVPPIETPSQFWKP 102

QY 80 IGLRLILQAR--YKAARNOATNAQIL 106
Db 103 LOYVSKVTDKCKSFYEKKNASHNAQKL 131

RESULT 14
MNZSP
nonstructural protein V - simian paramyxovirus SV5 (strain W3)
C/Species: simian paramyxovirus SV5
C/Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Jul-1999
C/Accession: A31594
R/Thomas, S.M.; Lamb, R.A.; Paterson, R.G.
Cell 54, 891-902, 1988
A/Title: Two mRNAs that differ by two nontemplated nucleotides encode the amino cotermin
A/Reference number: A90902; MUID:88311091; PMID:3044614
A/Accession: A31594
A/Molecule type: mRNA
A/Residues: 1-222 <THO>
A/Cross-references: GB:J03142; NID:g335118; PIDN:AAA47882.1; PID:g335119
C/Genetics:
A/Gene: V

Query Match 12.8%; Score 71.5; DB 1; Length 222;
Best Local Similarity 32.3%; Pred. No. 8.9;
Matches 31; Conservative 9; Mismatches 29; Indels 27; Gaps 5;
QY 20 VPGTPIPTFOLLPONSLETPSSVTSSSGTTGTPSASWSNSKASPY----LDTRVILS 75
Db 93 VPGKPIPN----PLGLDSTPTQTVDLSGKTL-PSGSYKGVKGLAKFGKENLMTTFI-- 145

QY 76 LDVPIGLRLILQAR--YKAARNOATNAQILAHVGR 111
Db 146 -----EEPR-----ENPIATSSPIDFKRGR 165

RESULT 15
T29689
hypothetical protein ZC266.2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Sep-2000
C/Accession: T29689
R/Du, Z.; Kemp, K.; Scheet, P.
submitted to the EMBL Data Library, March 1996
A/Description: The sequence of C. elegans cosmid ZC266.
A/Reference number: Z20665
A/Accession: T29689
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA

A:Residues: 1-276 <DUZ>
A/Cross-references: EMBL:U53140; PIDN:AAA96101.1; GSPDB:GN00023; CESP:ZC266.2
A/Experimental source: strain Bristol N2; clone ZC266
C/Genetics:
A/Gene: CESP:ZC266.2
A/Map position: 5
A/Introns: 40/3; 66/1; 100/3; 133/1; 165/2
C/Superfamily: Caenorhabditis elegans hypothetical protein ZC266.2

Query Match 12.8; Score 71.5; DB 2; Length 276;
Best local Similarity 30.5%; Pred. No. 12;
Matches 29; Conservative 13; Mismatches 38; Indels 15; Gaps 4;

QY 18 LFVPGTPIPTFQLLPONSLETPSSVTSSSG-TTTPSASWSNKGAPYLDTRVI--- 73
Db 126 VYSEGCPSPDSSLKPFSSANVTISK--SRTSNGEVTISSSSYSRSKRQYL--RVLRR 181

QY 74 -----LSLDVPGLRLLEQARYKAARNQAT 101
Db 182 LCITFDLSMNLPSYLLRLYLSLSNEPVTBEWAET 216

Search completed: April 20, 2004, 18:57:22
Job time : 22.16 secs

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OM protein - protein search, using sw model

Run on: April 20, 2004, 18:50:27 ; Search time 74.6667 Seconds
(without alignments)
423.821 Million cell updates/sec

Title: US-09-919-473-10
Perfect score: 557
Sequence: 1 MTRWLVVFWVLMRLFLV.....KARNQATNAQILAHVGR 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	557	100.0	112	5 AAE21008	Aae21008 Mouse uro
2	312	56.0	112	5 AAE21006	Aae21006 Human uro
3	312	56.0	112	5 AAO15170	Aao15170 Human str
4	179	32.1	38	5 AAO19441	Aao19441 Murine ur
5	179	32.1	38	5 ABB82357	Abb82357 Mouse uro
6	145	26.0	41	5 AAE21007	Aae21007 Human mat
7	140	25.1	38	7 ADE64811	Ade64811 Corticotr
8	140	25.1	38	7 ADE51097	Ade51097 CRF2 non-
9	139	25.0	38	5 AAE21009	Aae21009 Human uro
10	139	25.0	38	5 AAO19442	Aao19442 Human uro
11	139	25.0	38	5 ABB82356	Abb82356 Human uro
12	139	25.0	38	7 ADE64820	Ade64820 Corticotr
13	139	25.0	38	7 ADE64701	Ade64701 CRF-2 rel
14	139	25.0	38	7 ADE65051	Ade65051 Corticotr
15	139	25.0	38	7 ADE51106	Ade51106 CRF2 non-
16	139	25.0	38	7 ADE51337	Ade51337 CRF2 huma
17	139	25.0	38	7 ADE50987	Ade50987 CRF2 non-
18	139	25.0	39	7 ADE65065	Ade65065 Corticotr
19	139	25.0	39	7 ADE65053	Ade65053 Corticotr
20	139	25.0	39	7 ADE51351	Ade51351 CRF2 non-
21	139	25.0	39	7 ADE51339	Ade51339 CRF2 non-
22	138	24.8	38	7 ADE64819	Ade64819 Corticotr
23	138	24.8	38	7 ADE51105	Ade51105 CRF2 non-
24	137	24.6	38	7 ADE64807	Ade64807 Corticotr
25	137	24.6	38	7 ADE51093	Ade51093 CRF2 non-

26	136	24.4	38	7 ADE64824	Ade64824 Corticotr
27	136	24.4	38	7 ADE64827	Ade64827 Corticotr
28	136	24.4	38	7 ADE64806	Ade64806 Corticotr
29	136	24.4	38	7 ADE64821	Ade64821 Corticotr
30	136	24.4	38	7 ADE51113	Ade51113 CRF2 non-
31	136	24.4	38	7 ADE51092	Ade51092 CRF2 non-
32	136	24.4	38	7 ADE51110	Ade51110 CRF2 non-
33	136	24.4	38	7 ADE51107	Ade51107 CRF2 non-
34	135	24.2	38	7 ADE64808	Ade64808 Corticotr
35	135	24.2	38	7 ADE64809	Ade64809 Corticotr
36	135	24.2	38	7 ADE64817	Ade64817 Corticotr
37	135	24.2	38	7 ADE64825	Ade64825 Corticotr
38	135	24.2	38	7 ADE51111	Ade51111 CRF2 non-
39	135	24.2	38	7 ADE51094	Ade51094 CRF2 non-
40	135	24.2	38	7 ADE51095	Ade51095 CRF2 non-
41	135	24.2	38	7 ADE51103	Ade51103 CRF2 non-
42	135	24.2	44	7 ADE64993	Ade64993 Corticotr
43	135	24.2	44	7 ADE51279	Ade51279 CRF2 non-
44	134	24.1	38	7 ADE64816	Ade64816 Corticotr
45	134	24.1	38	7 ADE64815	Ade64815 Corticotr

ALIGNMENTS

RESULT 1
AAE21008
ID AAE21008 standard; protein; 112 AA.

XX AAE21008;

AC AAE21008;

DT 01-JUL-2002 (first entry)

XX Mouse urocortin II (ucn) protein.

DE Mouse; urocortin-related peptide; URP; antipyretic; cardiant; urocortin;

KW ucn; tranquilliser; appetite dysfunction; congestive heart failure;

KW stress; anxiety.

XX Mus musculus.

XX WO200212307-A1.

XX 14-FEB-2002.

PF 31-JUL-2001; 2001WO-US023976.

PR 04-AUG-2000; 2000US-0223255P.

PR 07-MAR-2001; 2001US-0273969P.

XX (RERE-) RES DEV FOUND.

PI Vale WW, Sawchenko PF, Lewis KA, Vaughan JM, Reyes TM, Rivier JB;

PI Hogenesch JB, Perrin MH;

XX WPI; 2002-241737/29.

XX Novel urocortin II polypeptide or human urocortin-related peptide, for

PT treating high body temperature, appetite dysfunction, congestive heart

PT failure, stress, anxiety and low levels of adrenocortico tropic hormone.

XX Claim 2; Fig 4A; 94pp; English.

XX The invention relates to a modified protein selected from urocortin II

CC (Ucn II) and human urocortin-related peptide (URP). A pharmaceutical

CC composition is useful for treating a pathophysiological state including

CC high body temperature, appetite dysfunction, congestive heart failure,

CC stress, anxiety and undesirably low levels of adrenocortico tropic

CC hormone (ACTH) secretions. A modified protein conjugate is useful in

CC scintigraphy and in various assays, and also for the targeted

CC destruction of Corticotropin-releasing factor (CRF) receptor bearing

CC cells. The present sequence is mouse urocortin II (ucn) protein

SQ Sequence 112 AA;

Query Match 100.0%; Score 557; DB 5; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.9e-54;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRWLVVVFVLMRLIFVPGTPIPTFOLLQNSLETTPSSVTSESSSGTTTGPASWS 60
 DB 1 MTRWLVVVFVLMRLIFVPGTPIPTFOLLQNSLETTPSSVTSESSSGTTTGPASWS 60
 QY 61 NSKASPYLDTRVILSLDVPILGLRLLEQARYKAARNOATNAQILAHVGR 112
 DB 61 NSKASPYLDTRVILSLDVPILGLRLLEQARYKAARNOATNAQILAHVGR 112

RESULT 2

AAE21006
 ID AAE21006 standard; protein; 112 AA.

AC AAE21006;

DT 01-JUL-2002 (first entry)

DE Human urocortin-related peptide (URP) protein.

KW Human; urocortin-related peptide; URP; antipyrretic; cardiant; urocortin;
 KW ucn; tranquilliser; appetite dysfunction; congestive heart failure;
 KW stress; anxiety.

OS Homo sapiens.

Key Location/Qualifiers
 FH Peptide 1..19
 FT /label= Signal_peptide
 FT Protein 72..112
 FT /label= Mature_URP_protein
 FT Modified-site 112
 FT /note= "C-terminal amide"

WO200212307-A1.

14-FEB-2002.

31-JUL-2001; 2001WO-US023976.

04-AUG-2000; 2000US-0223255P.

07-MAR-2001; 2001US-0273969P.

(RERE-) RES DEV FOUND.

Vale WW, Sawchenko PF, Lewis KA, Vaughan JM, Reyes TM, Rivier JE;
 Hogenesch JB, Perrin MH;

WPI; 2002-241737/29.

N-PSDB; AAD33401.

Novel urocortin II polypeptide or human urocortin-related peptide, for
 treating high body temperature, appetite dysfunction, congestive heart
 failure, stress, anxiety and low levels of adrenocortico tropic hormone.

Claim 18; Fig 1; 94pp; English.

The invention relates to a modified protein selected from urocortin II
 (Ucn II) and human urocortin-related peptide (URP). A pharmaceutical
 composition is useful for treating a pathophysiological state including
 high body temperature, appetite dysfunction, congestive heart failure,
 stress, anxiety and undesirably low levels of adrenocortico tropic
 hormone (ACTH) secretions. A modified protein conjugate is useful in
 scintigraphy and in various assays, and also for the targeted
 destruction of Corticotropin-releasing factor (CRF) receptor bearing
 cells. The present sequence is human URP protein

Sequence 112 AA;

Query Match 56.0%; Score 312; DB 5; Length 112;
 Best Local Similarity 60.9%; Pred. No. 5.7e-27;
 Matches 67; Conservative 15; Mismatches 28; Indels 0; Gaps 0;

QY 1 MTRWLVVVFVLMRLIFVPGTPIPTFOLLQNSLETTPSSVTSESSSGTTTGPASWS 60
 DB 1 MTRCALLMLMLGRVLVFPVPTPTFQLRPQNSPQTPRPAASESPSAAPTWPAAQS 60

QY 61 NSKASPYLDTRVILSLDVPILGLRLLEQARYKAARNOATNAQILAHVG 110

DB 61 HCSPTRHFGSRIVLSLDVPILGLQLLEQARARAREQATTNARILARVG 110

RESULT 3

AAO15170

ID AAO15170 standard; protein; 112 AA.

AC AAO15170;

DT 02-SEP-2002 (first entry)

DE Human stresscopin 1 protein.

KW Human; stresscopin 1; weight reduction; gene therapy;
 KW corticotropin releasing hormone receptor 2 activator; CRH-R2 activator;
 KW appetite suppression; cardioprotection; inflammation; heart disease;
 KW organ graft rejection; hypertension; trauma stress; dysthymia; oedema;
 KW skin disease; inflammatory arthritis; rheumatoid arthritis;
 KW non-infectious inflammatory arthropathy; stress-related disorder.

OS Homo sapiens.

Key Location/Qualifiers
 FH Peptide 1..66
 FT /label= Signal_peptide
 FT Protein 67..112
 FT /note= "Mature stresscopin 1 protein"
 FT Misc-difference 67..109
 FT /note= "This region is illegible in the specification and
 has been generated by decoding the corresponding
 nucleotide (AAL43490)"

WO200234934-A2.

02-MAY-2002.

10-OCT-2001; 2001WO-US032065.

26-OCT-2000; 2000US-0244128P.

15-MAR-2001; 2001US-0276615P.

(STRD) UNIV LELAND STANFORD JUNIOR.

Hsu SY, Hsueh AJW;

WPI; 2002-471444/50.

N-PSDB; AAL43490.

Composition comprising human stresscopin 1 or stresscopin 2 polypeptide,
 useful in appetite suppression, for cardioprotection, reducing edema,
 reducing inflammation, organ graft rejection, reducing hypertension.

Claim 2; Fig 1A; 50pp; English.

The invention comprises the amino acid and coding sequences of two human
 proteins which activate the corticotropin releasing hormone receptor 2
 (CRH-R2). The proteins of the invention are called stresscopin 1 and
 stresscopin 2. The stresscopin DNA and protein sequences of the invention
 are useful for appetite suppression, cardioprotection, reducing edema,
 reducing inflammation, reducing organ graft rejection, reducing
 hypertension and reducing trauma stress. The stresscopin DNA and protein
 sequences are also useful for the treatment of dysthymia, skin diseases,

CC inflammatory arthritis, non-infectious inflammatory arthropathy (e.g.
 CC rheumatoid arthritis), heart disease and stress-related disorders. The
 CC present amino acid sequence represents the human stresscopin 1 protein
 XX
 SQ Sequence 112 AA;
 Query Match 56.0%; Score 312; DB 5; Length 112;
 Best Local Similarity 60.9%; Pred. No. 5.7e-27;
 Matches 67; Conservative 15; Mismatches 28; Indels 0; Gaps 0;
 QY 1 MTRWLVFVFLMLDRLLFVPGTPIPTFOLLPNSLETTPSSVTSSSGTTTGPSASWS 60
 DB 1 MTRCALLMLVLMGLRVLVVPTPIPTFQRPNSQPTTPRPAASPSAAATWFWAQS 60
 QY 61 NKSASPYLDNRVILSDVPICGLRILILEQARYKAARNQAATNAQILAHV 110
 DB 61 HCSFTRHPSGRIVLSLDVPICGLILILEQARARAAREQATTNARILARVG 110
 RESULT 4
 ID AAO19441 standard; peptide; 38 AA.
 AC AAO19441;
 DT 10-DEC-2002 (first entry)
 DE Murine urocortin II.
 KW Human; rat; mouse; sheep; cow; chicken; CRF1R; CRF2R;
 KW skeletal muscle atrophy; corticotrophin releasing factor-2 receptor;
 KW muscular dystrophy; corticotrophin releasing factor-1 receptor;
 KW gene therapy.
 XX Mus musculus.
 OS WO200269908-A2.
 PN 12-SEP-2002.
 PD 06-MAR-2002; 2002WO-US007476.
 PF 06-MAR-2001; 2001US-00799978.
 PR (PROC) PROCTER & GAMBLE CO.
 PA Isfort RJ, Sheldon RJ;
 PI WPI; 2002-713413/77.
 DR Identifying candidate compounds for regulating skeletal muscle mass or
 PT treating skeletal muscle atrophy by identifying test compounds that bind
 PT to, or activate, the corticotropin releasing factor-2 receptor.
 XX Disclosure; Page 164; 167pp; English.
 PS The present invention relates to a method of identifying candidate
 CC compounds for regulating skeletal muscle mass or function, and comprises
 CC contacting a test compound with a corticotropin releasing factor-2
 CC receptor (CRF2R) or with a cell expressing a functional CRF2R,
 CC determining whether the test compound binds to, or activates, the CRF2R
 CC and identifying the test compounds that bind to, or activates, the CRF2R
 CC as candidate compounds for regulating skeletal muscle mass or function.
 CC The method is useful for preparing a medicament for treating skeletal
 CC muscle atrophy or for prophylactic treatment of muscular dystrophies. The
 CC present sequence is a murine peptide shown in the invention
 XX Sequence 38 AA;
 Query Match 32.1%; Score 179; DB 5; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.2e-12;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 72 VILSDVPICGLRILILEQARYKAARNQAATNAQILAHV 109
 DB 1 VILSDVPICGLRILILEQARYKAARNQAATNAQILAHV 38
 RESULT 6
 ID AAE21007 standard; peptide; 41 AA.
 AC AAE21007;
 DT 01-JUL-2002 (first entry)
 XX Human mature urocortin-related peptide (URP).
 DE
 XX

QY 72 VILSDVPICGLRILILEQARYKAARNQAATNAQILAHV 109
 DB 1 VILSDVPICGLRILILEQARYKAARNQAATNAQILAHV 38
 RESULT 5
 ID ABB82357 standard; protein; 38 AA.
 AC ABB82357;
 DT 08-JAN-2003 (first entry)
 DE Mouse urocortin II protein (UcnII) fragment.
 KW Urocortin III; Ucn-III; cardiant; antidiabetic; antimigraine; mouse;
 KW tranquilliser; antipyretic; vasotropic; gastrointestinal; antiangiogenic;
 KW vaccine; urocortin II; UcnII.
 XX Mus musculus.
 OS WO200274326-A2.
 PN 26-SEP-2002.
 PD 15-MAR-2002; 2002WO-US009115.
 PF 15-MAR-2001; 2001US-0276069P.
 PR 31-MAY-2001; 2001US-0294914P.
 PA (RERE-) RES DEV FOUND.
 PI Vale WM, Rivier JE, Kunitake KS, Lewis KA, Perrin MH, Gulyas J;
 XX WPI; 2002-740838/80.
 DR New human or mouse urocortin III protein, useful e.g. for treating
 PT congestive heart failure, vascular disease, gastrointestinal dysfunction,
 PT diabetes mellitus, high temperature, appetite dysfunction and stress.
 XX Example; Fig 2C; 81pp; English.
 PS The invention relates to an isolated and purified human or mouse
 CC urocortin III (Ucn-III) protein. The Ucn-III protein is useful: (i)
 CC for treating a pathophysiological state including congestive heart
 CC failure, vascular disease, gastrointestinal dysfunction, diabetes
 CC mellitus, high temperature, appetite dysfunction, stress, undesirably low
 CC levels of glucagon secretion or activity, anxiety and migraine headaches;
 CC (ii) for determining whether a cell has urocortin III receptors; and
 CC (iii) for inhibiting angiogenesis. The present sequence represents the
 CC mouse urocortin II protein fragment
 XX Sequence 38 AA;
 Query Match 32.1%; Score 179; DB 5; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.2e-12;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 72 VILSDVPICGLRILILEQARYKAARNQAATNAQILAHV 109
 DB 1 VILSDVPICGLRILILEQARYKAARNQAATNAQILAHV 38
 RESULT 6
 ID AAE21007 standard; peptide; 41 AA.
 AC AAE21007;
 DT 01-JUL-2002 (first entry)
 XX Human mature urocortin-related peptide (URP).
 DE
 XX

PN WO2003062268-A2.
 XX 31-JUL-2003.
 PD 16-JAN-2003; 2003WO-US001451.
 XX 16-JAN-2002; 2002US-0349117P.
 XX 29-APR-2002; 2002US-0376337P.
 PR 14-JUN-2002; 2002US-0388955P.
 PR 19-SEP-2002; 2002US-0411988P.
 XX (PROC) PROCTER & GAMBLE CO.
 PA Isfort RJ, Mazur WA;
 XX WPI; 2003-787974/74.
 XX New non-native peptide derived from corticotropin-releasing factor-2,
 PT useful for treatment and prevention of e.g. muscular atrophy, also
 PT related nucleic acid and antibodies.
 XX Example 2; SEQ ID NO 114; 300pp; English.
 PS The invention relates to a novel non-native peptide derived from
 CC corticotropin-releasing factor-2 (CRF2). The non-native CRF2 peptides
 CC have the following activities: myopathic, osteopathic, hypotensive,
 CC cardiant, vasotropic, antimigraine, cerebroprotective, nootropic,
 CC neuroprotective, anorectic, antidiabetic, analgesic, antiallergic,
 CC tranquilizer, anxiolytic, antidepressant, and antiarthritic. The non-
 CC native CRF2 peptides, and related compounds derived from other proteins,
 CC are used to prevent or treat disorders modulated by the CRF2 receptor,
 CC e.g. skeletal muscle atrophy or wasting, and bone disorders, however
 CC caused; heart/circulatory diseases (e.g. hypertension, congestive heart
 CC failure, heart attack, reperfusion injury, migraine, stroke, memory loss,
 CC Alzheimer's diseases, dementia); joint disorders (osteoarthritis or
 CC rheumatoid arthritis); metabolic disease (obesity or diabetes); pain;
 CC allergy; stress; anxiety; low levels of adrenocorticotrophic hormone;
 CC anorexia nervosa; depression; also to reduce body temperature and to
 CC control appetite or cognitive function. Nucleic acids, optionally
 CC labelled, that encode the non-native CRF2 peptides are used as primers
 CC and probes for amplification, also for gene synthesis and for recombinant
 CC production of the non-native CRF2 peptides, including use in gene
 CC therapy. Antibodies specific for the non-native CRF2 peptides are used to
 CC evaluate expression of the non-native CRF2 peptides after gene therapy.
 CC This sequence represents a CRF2 non-native polypeptide of the invention.
 XX
 SQ Sequence 38 AA;
 Query Match 25.1%; Score 140; DB 7; Length 38;
 Best Local Similarity 76.3%; Pred. No. 2.8e-08;
 Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 72 VILSLDVPILGLRLLEQARYKAAARNQAAATNAQILAHV 109
 DB 1 IVLSLDVPILGLQLLEQARARAREQATTNARILARV 38
 RESULT 9
 AAE21009
 ID AAE21009 standard; peptide; 38 AA.
 XX AAE21009;
 AC AAE21009;
 XX 01-JUL-2002 (first entry)
 DT Human urocortin-related peptide (URP).
 DE Human; urocortin-related peptide; URP; antipyretic; cardiant; urocortin;
 KW ucn; tranquilliser; appetite dysfunction; congestive heart failure;
 KW stress; anxiety.
 XX Homo sapiens.
 OS Homo sapiens.

FH Key Location/Qualifiers
 FT Modified-site 38
 FT /note= "C-terminal amide"
 XX WO2000212307-A1.
 FN 14-FEB-2002.
 PD 31-JUL-2001; 2001WO-US023976.
 XX 04-AUG-2000; 2000US-0223255P.
 PR 07-MAR-2001; 2001US-0273969P.
 XX (RERE-) RES DEV FOUND.
 PA Vale WW, Sawchenko PF, Lewis KA, Vaughan JM, Reyes TM, Rivier JE;
 PI Hogeneesch JB, Perrin MH;
 PI WPI; 2002-241737/29.
 DR Novel urocortin II polypeptide or human urocortin-related peptide, for
 XX treating high body temperature, appetite dysfunction, congestive heart
 PT failure, stress, anxiety and low levels of adrenocortico tropic hormone.
 PS Claim 36; Fig 4b; 94pp; English.
 CC The invention relates to a modified protein selected from urocortin II
 CC (Ucn II) and human urocortin-related peptide (URP). A pharmaceutical
 CC composition is useful for treating a pathophysiological state including
 CC high body temperature, appetite dysfunction, congestive heart failure,
 CC stress, anxiety and undesirably low levels of adrenocortico tropic
 CC hormone (ACTH) secretions. A modified protein conjugate is useful in
 CC scintigraphy and in various assays, and also for the targetted
 CC destruction of corticotropin-releasing factor (CRF) receptor bearing
 CC cells. The present sequence is human URP
 SQ Sequence 38 AA;
 Query Match 25.0%; Score 139; DB 5; Length 38;
 Best Local Similarity 76.3%; Pred. No. 3.6e-08;
 Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 72 VILSLDVPILGLRLLEQARYKAAARNQAAATNAQILAHV 109
 DB 1 IVLSLDVPILGLQLLEQARARAREQATTNARILARV 38
 RESULT 10
 AAO19442
 ID AAO19442 standard; peptide; 38 AA.
 XX AAO19442;
 AC AAO19442;
 XX 10-DEC-2002 (first entry)
 DT Human urocortin-related peptide.
 DE Human; rat; mouse; sheep; cow; chicken; CRF1R; CRF2R;
 KW skeletal muscle atrophy; corticotrophin releasing factor-2 receptor;
 KW muscular dystrophy; corticotrophin releasing factor-1 receptor;
 KW gene therapy.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO200269908-A2.
 PD 12-SEP-2002.
 XX 06-MAR-2002; 2002WO-US007476.
 XX 06-MAR-2001; 2001US-00799978.
 XX (PROC) PROCTER & GAMBLE CO.

The invention relates to a novel non-native peptide derived from corticotropin-releasing factor-2 (CRF2). The CRF2 peptides have the following activities: myopathic, osteopathic, hypertensive, cardiac, vasotropic, antimigraine, cerebroprotective, nootropic, neuroprotective, anesthetic, antidiabetic, analgesic, antiallergic, tranquilizer, anxiolytic, antidepressant, and antiarthritic. The CRF2 peptides, and related compounds derived from other proteins, are used to prevent or treat disorders modulated by the CRF2 receptor, e.g. skeletal muscle atrophy or wasting, and bone disorders, however caused; heart/circulatory diseases (e.g. hypertension, congestive heart failure, heart attack, reperfusion injury, migraine, stroke, memory loss, Alzheimer's disease, dementia); joint disorders (osteoarthritis or rheumatoid arthritis); metabolic disease (obesity or diabetes); pain; allergy; stress; anxiety; low levels of adrenocorticotrophic hormone; anorexia nervosa; depression;

CC also to reduce body temperature and to control appetite or cognitive
 CC function. Nucleic acids, optionally labelled, that encode the CRF2
 CC peptides are used as primers and probes for amplification, also for gene
 CC synthesis and for recombinant production of CRF2 peptides, including use
 CC in gene therapy. Antibodies specific for the CRF2 peptides are used to
 CC evaluate expression of the CRF2 peptides after gene therapy. This
 CC sequence represents a novel native CRF polypeptide of the invention.
 XX
 SQ Sequence 38 AA;

Query Match 25.0%; Score 139; DB 7; Length 38;
 Best Local Similarity 76.3%; Pred. No. 3.6e-08;
 Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 72 VILSDVPVIGLLRILLEQARYKAARNQAATNAQILAHV 109
 Db 1 IVLSLDVPVIGLLRILLEQARQEAAREQATTNARILARV 38

RESULT 13
 ADE64701
 ID ADE64701 standard; peptide; 38 AA.
 XX AC ADE64701;
 XX DT 29-JAN-2004 (first entry)
 XX DE CRP-2 related human urocortin II polypeptide, SEQ ID No 4.
 XX KW corticotropin-releasing factor-2; CRF2; myopathic; osteopathic;
 KW hypotensive; cardiant; vasotropic; antimigraine; cerebroprotective;
 KW nootropic; neuroprotective; anorectic; antidiabetic; analgesic;
 KW antiallergic; tranquilizer; anxiolytic; antidepressant; antiarthritic;
 KW gene therapy; human.
 XX OS Homo sapiens.
 XX FN WO2003062277-A1.
 XX PD 31-JUL-2003.
 XX PF 16-JAN-2003; 2003WO-US001454.
 XX PR 16-JAN-2002; 2002US-0349117P.
 XX PR 29-APR-2002; 2002US-0376337P.
 XX PR 14-JUN-2002; 2002US-038895P.
 XX PR 19-SEP-2002; 2002US-0411988P.
 XX PA (PROC) PROCTER & GAMBLE CO.
 XX PI Isfort RJ, Mazur WA;
 XX DR WPI; 2003-787975/74.
 XX PT New non-native peptide derived from corticotropin-releasing factor-2,
 XX useful for treatment and prevention of e.g. muscular atrophy, also
 XX related nucleic acid and antibodies.
 XX PS Example 1; SEQ ID NO 4; 304pp; English.

XX The invention relates to a novel non-native peptide derived from
 CC corticotropin-releasing factor-2 (CRF2). The CRF2 peptides have the
 CC following activities: myopathic, osteopathic, hypotensive, cardiant,
 CC vasotropic, antimigraine, cerebroprotective, nootropic, neuroprotective,
 CC anorectic, antidiabetic, analgesic, antiallergic, tranquilizer,
 CC anxiolytic, antidepressant, and antiarthritic. The CRF2 peptides, and
 CC related compounds derived from other proteins, are used to prevent or
 CC treat disorders modulated by the CRF2 receptor, e.g. skeletal muscle
 CC atrophy or wasting, and bone disorders, however caused; heart/circulatory
 CC diseases (e.g. hypertension, congestive heart failure, heart attack,
 CC reperfusion injury, migraine, stroke, memory loss, Alzheimer's disease,
 CC dementia); joint disorders (osteoarthritis or rheumatoid arthritis);
 CC metabolic disease (obesity or diabetes); pain; allergy; stress; anxiety;

CC low levels of adrenocorticotrophic hormone; anorexia nervosa; depression;
 CC also to reduce body temperature and to control appetite or cognitive
 CC function. Nucleic acids, optionally labelled, that encode the CRF2
 CC peptides are used as primers and probes for amplification, also for gene
 CC synthesis and for recombinant production of CRF2 peptides, including use
 CC in gene therapy. Antibodies specific for the CRF2 peptides are used to
 CC evaluate expression of the CRF2 peptides after gene therapy. This
 CC sequence represents a novel native CRF polypeptide of the invention.
 XX
 SQ Sequence 38 AA;

Query Match 25.0%; Score 139; DB 7; Length 38;
 Best Local Similarity 76.3%; Pred. No. 3.6e-08;
 Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 72 VILSDVPVIGLLRILLEQARYKAARNQAATNAQILAHV 109
 Db 1 IVLSLDVPVIGLLRILLEQARQEAAREQATTNARILARV 38

RESULT 14
 ADE65051
 ID ADE65051 standard; peptide; 38 AA.
 XX AC ADE65051;
 XX DT 29-JAN-2004 (first entry)
 XX DE Corticotropin-releasing factor-2 polypeptide, SEQ ID No 354.
 XX KW corticotropin-releasing factor-2; CRF2; myopathic; osteopathic;
 KW hypotensive; cardiant; vasotropic; antimigraine; cerebroprotective;
 KW nootropic; neuroprotective; anorectic; antidiabetic; analgesic;
 KW antiallergic; tranquilizer; anxiolytic; antidepressant; antiarthritic;
 KW gene therapy.
 XX OS Unidentified.
 XX FN WO2003062277-A1.
 XX PD 31-JUL-2003.
 XX PF 16-JAN-2003; 2003WO-US001454.
 XX PR 16-JAN-2002; 2002US-0349117P.
 XX PR 29-APR-2002; 2002US-0376337P.
 XX PR 14-JUN-2002; 2002US-038895P.
 XX PR 19-SEP-2002; 2002US-0411988P.
 XX PA (PROC) PROCTER & GAMBLE CO.
 XX PI Isfort RJ, Mazur WA;
 XX DR WPI; 2003-787975/74.
 XX PT New non-native peptide derived from corticotropin-releasing factor-2,
 XX useful for treatment and prevention of e.g. muscular atrophy, also
 XX related nucleic acid and antibodies.
 XX PS Example 2; SEQ ID NO 354; 304pp; English.

XX The invention relates to a novel non-native peptide derived from
 CC corticotropin-releasing factor-2 (CRF2). The CRF2 peptides have the
 CC following activities: myopathic, osteopathic, hypotensive, cardiant,
 CC vasotropic, antimigraine, cerebroprotective, nootropic, neuroprotective,
 CC anorectic, antidiabetic, analgesic, antiallergic, tranquilizer,
 CC anxiolytic, antidepressant, and antiarthritic. The CRF2 peptides, and
 CC related compounds derived from other proteins, are used to prevent or
 CC treat disorders modulated by the CRF2 receptor, e.g. skeletal muscle
 CC atrophy or wasting, and bone disorders, however caused; heart/circulatory
 CC diseases (e.g. hypertension, congestive heart failure, heart attack,
 CC reperfusion injury, migraine, stroke, memory loss, Alzheimer's disease,
 CC dementia); joint disorders (osteoarthritis or rheumatoid arthritis);

CC metabolic disease (obesity or diabetes); pain; allergy; stress; anxiety;
 CC low levels of adrenocorticotrophic hormone; anorexia nervosa; depression;
 CC also to reduce body temperature and to control appetite or cognitive
 CC function. Nucleic acids, optionally labelled, that encode the CRF2
 CC peptides are used as primers and probes for amplification, also for gene
 CC synthesis and for recombinant production of CRF2 peptides, including use
 CC in gene therapy. Antibodies specific for the CRF2 peptides are used to
 CC evaluate expression of the CRF2 peptides after gene therapy. This
 CC sequence represents a novel native CRF polypeptide of the invention.
 XX
 XX Sequence 38 AA;
 SQ Query Match 25.0%; Score 139; DB 7; Length 38;
 Best Local Similarity 76.3%; Pred. No. 3.6e-08;
 Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 72 VILSLDVPILGLIRLLLEQARYKAARNQAATNAQILAHV 109
 Db 1 IVLSLDVPILGLIRLLLEQARARAREQATTNARILARV 38
 RESULT 15
 ADE51106
 ID ADE51106 standard; peptide; 38 AA.
 XX
 XX ADE51106;
 XX
 XX 29-JAN-2004 (first entry)
 XX
 XX CRF2 non-native polypeptide, SEQ ID NO 123.
 XX
 XX non-native; corticotropin-releasing factor-2; CRF2; myopathic;
 KW osteopathic; hypotensive; cardiant; vasotropic; antimigraine;
 KW cerebroprotective; nootropic; neuroprotective; anorectic; antidiabetic;
 KW analgesic; antiallergic; tranquilizer; anxiolytic; antidepressant;
 KW antiarthritic.
 XX
 XX Unidentified.
 OS
 XX
 XX WO2003062268-A2.
 FN
 XX
 XX 31-JUL-2003.
 PD
 XX
 XX 16-JAN-2003; 2003WO-US001451.
 PF
 XX
 XX 16-JAN-2002; 2002US-0349117P.
 PR
 XX
 XX 29-APR-2002; 2002US-0376337P.
 PR
 XX
 XX 14-JUN-2002; 2002US-0388895P.
 PR
 XX
 XX 19-SEP-2002; 2002US-0411988P.
 XX
 XX (PROC) PROCTER & GAMBLE CO.
 PA
 XX
 XX Isfort RJ, Mazur WA;
 PI
 XX
 XX WPI; 2003-787974/74.
 DR
 XX
 XX New non-native peptide derived from corticotropin-releasing factor-2,
 PT useful for treatment and prevention of e.g. muscular atrophy, also
 PT related nucleic acid and antibodies.
 XX
 XX Example 2; SEQ ID NO 123; 300pp; English.
 PS
 XX
 XX The invention relates to a novel non-native peptide derived from
 CC corticotropin-releasing factor-2 (CRF2). The non-native CRF2 peptides
 CC have the following activities: myopathic, osteopathic, hypotensive,
 CC cardiant, vasotropic, antimigraine, cerebroprotective, nootropic,
 CC neuroprotective, anorectic, antidiabetic, analgesic, antiallergic,
 CC tranquilizer, anxiolytic, antidepressant, and antiarthritic. The non-
 CC native CRF2 peptides, and related compounds derived from other proteins,
 CC are used to prevent or treat disorders modulated by the CRF2 receptor,
 CC e.g. skeletal muscle atrophy or wasting, and bone disorders, however
 CC caused; heart/circulatory diseases (e.g. hypertension, congestive heart
 CC failure, heart attack, reperfusion injury, migraine, stroke, memory loss,

CC Alzheimer's diseases, dementia); joint disorders (osteoarthritis or
 CC rheumatoid arthritis); metabolic disease (obesity or diabetes); pain;
 CC allergy; stress; anxiety; low levels of adrenocorticotrophic hormone;
 CC anorexia nervosa; depression; also to reduce body temperature and to
 CC control appetite or cognitive function. Nucleic acids, optionally
 CC labelled, that encode the non-native CRF2 peptides are used as primers
 CC and probes for amplification, also for gene synthesis and for recombinant
 CC production of the non-native CRF2 peptides, including use in gene
 CC therapy. Antibodies specific for the non-native CRF2 peptides are used to
 CC evaluate expression of the non-native CRF2 peptides after gene therapy.
 CC This sequence represents a CRF2 non-native polypeptide of the invention.
 XX
 XX Sequence 38 AA;
 SQ Query Match 25.0%; Score 139; DB 7; Length 38;
 Best Local Similarity 76.3%; Pred. No. 3.6e-08;
 Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 72 VILSLDVPILGLIRLLLEQARYKAARNQAATNAQILAHV 109
 Db 1 IVLSLDVPILGLIRLLLEQARARAREQATTNARILARV 38

Search completed: April 20, 2004, 18:54:43
 Job time : 75.6667 secs

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OM protein - protein search, using sw model

Run on: April 20, 2004, 18:50:27 / Search time 25.3333 Seconds
(without alignments)
423.821 Million cell updates/sec

Title: US-09-919-473-11
Perfect score: 179
Sequence: 1 VILSDVPIGLRILLEQARYKARNQATNAQILAHV 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	179	100.0	38	5	AAO19441 Murine ur
2	179	100.0	38	5	ABB82357 Mouse uro
3	179	100.0	112	5	AAE21008 Mouse uro
4	140	78.2	38	7	ADE64811 Corticotr
5	140	78.2	38	7	ADE51097 CRF2 non-
6	139	77.7	38	5	AAE21009 Human uro
7	139	77.7	38	5	AAO19442 Human uro
8	139	77.7	38	5	ABB82356 Human uro
9	139	77.7	38	7	ADE64820 Corticotr
10	139	77.7	38	7	ADE64701 CRF-2 rel
11	139	77.7	38	7	ADE65051 Corticotr
12	139	77.7	38	7	ADE51106 CRF2 non-
13	139	77.7	38	7	ADE51337 CRF2 non-
14	139	77.7	38	7	ADE50987 CRF2 huma
15	139	77.7	39	7	ADE65065 Corticotr
16	139	77.7	39	7	ADE65053 Corticotr
17	139	77.7	39	7	ADE51351 CRF2 non-
18	139	77.7	39	7	ADE51339 CRF2 non-
19	139	77.7	41	5	AAE21006 Human mat
20	139	77.7	112	5	AAE21006 Human uro
21	139	77.7	112	5	AAO15170 Human str
22	138	77.1	38	7	ADE64819 Corticotr
23	138	77.1	38	7	ADE51105 CRF2 non-
24	137	76.5	38	7	ADE64807 Corticotr
25	137	76.5	38	7	ADE51093 CRF2 non-

26	136	76.0	38	7	ADE64824 Corticotr
27	136	76.0	38	7	ADE64827 Corticotr
28	136	76.0	38	7	ADE64806 Corticotr
29	136	76.0	38	7	ADE64821 Corticotr
30	136	76.0	38	7	ADE51113 CRF2 non-
31	136	76.0	38	7	ADE51092 CRF2 non-
32	136	76.0	38	7	ADE51110 CRF2 non-
33	136	76.0	38	7	ADE51107 CRF2 non-
34	135	75.4	38	7	ADE64808 Corticotr
35	135	75.4	38	7	ADE64809 Corticotr
36	135	75.4	38	7	ADE64817 Corticotr
37	135	75.4	38	7	ADE64825 Corticotr
38	135	75.4	38	7	ADE51111 CRF2 non-
39	135	75.4	38	7	ADE51094 CRF2 non-
40	135	75.4	38	7	ADE51095 CRF2 non-
41	135	75.4	38	7	ADE51103 CRF2 non-
42	135	75.4	44	7	ADE64993 Corticotr
43	135	75.4	44	7	ADE51279 CRF2 non-
44	134	74.9	38	7	ADE64816 Corticotr
45	134	74.9	38	7	ADE64815 Corticotr

ALIGNMENTS

RESULT 1
AAO19441
ID AAO19441 standard; peptide; 38 AA.
XX AAO19441;

DT 10-DEC-2002 (first entry)
XX Murine urocortin II.

XX Human; rat; mouse; sheep; cow; chicken; CRF1R; CRF2R;
KW skeletal muscle atrophy; corticotrophin releasing factor-2 receptor;
KW muscular dystrophy; corticotrophin releasing factor-1 receptor;
XX gene therapy.

OS Mus musculus.

XX WO200269908-A2.

XX 12-SEP-2002.

XX 06-MAR-2002; 2002WO-US007476.

XX 06-MAR-2001; 2001US-00799978.

XX (PROC) PROCTER & GAMBLE CO.

XX Isfort RJ, Sheldon RJ;

XX WPI; 2002-713413/77.

Identifying candidate compounds for regulating skeletal muscle mass or treating skeletal muscle atrophy by identifying test compounds that bind to, or activate, the corticotrophin releasing factor-2 receptor.

Disclosure; Page 164; 167pp; English.

The present invention relates to a method of identifying candidate compounds for regulating skeletal muscle mass or function, and comprises contacting a test compound with a corticotrophin releasing factor-2 receptor (CRF2R) or with a cell expressing a functional CRF2R, determining whether the test compound binds to, or activates, the CRF2R and identifying the test compounds that bind to, or activate, the CRF2R as candidate compounds for regulating skeletal muscle mass or function. The method is useful for prophylactic treatment of muscular dystrophies. The muscle atrophy or for prophylactic treatment of muscular dystrophies. The present sequence is a murine peptide shown in the invention

AC	AEE21008;
XX	
DT	01-JUL-2002 (first entry)
XX	
DE	Mouse urocortin II (ucn) protein.
XX	
KW	Mouse; urocortin-related peptide; URP; antipyretic; cardiant; urocortin;
XX	ucn; tranquilliser; appetite dysfunction; congestive heart failure;
KW	stress; anxiety.
XX	
OS	Mus musculus.
XX	
PN	WO200212307-A1.
XX	
PD	14-FEB-2002.
XX	
PF	31-JUL-2001; 2001WO-US023976.
XX	
PR	04-AUG-2000; 2000US-0223255P.
XX	07-MAR-2001; 2001US-0273969P.
XX	(RERE-) RES DEV FOUND.
XX	Vale WM, Sawchenko PF, Lewis KA, Vaughan JM, Reyes TM, Rivier JE;
PI	Hogensesch JB, Perrin MH;
XX	WPI; 2002-241737/29.
DR	
XX	Novel urocortin II polypeptide or human urocortin-related peptide, for
PFT	treating high body temperature, appetite dysfunction, congestive heart
PT	failure, stress, anxiety and low levels of adrenocortico tropic hormone
XX	Claim 2; Fig 4A; 94pp; English.
XX	The invention relates to a modified protein selected from urocortin II
CC	(Ucn II) and human urocortin-related peptide (URP). A pharmaceutical
CC	composition is useful for treating a pathophysiological state including
CC	high body temperature, appetite dysfunction, congestive heart failure,
CC	stress, anxiety and undesirably low levels of adrenocortico tropic
CC	hormone (ACTH) secretions. A modified protein conjugate is useful in
CC	scintigraphy and in various assays, and also for the targeted
CC	destruction of Corticotropin-releasing factor (CRF) receptor bearing
CC	cells. The present sequence is mouse urocortin II (ucn) protein
XX	
SQ	Sequence 112 AA;
	Query Match 100.0%; Score 179; DB 5; Length 112;
	Best Local Similarity 100.0%; Pred. No. 5.7e-21;
	Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps
QY	1 VILSDVPVIGLRLLEEQARYKAARNQAATNAQIIAHV 38
Dd	72 VILSDVPVIGLRLLEEQARYKAARNQAATNAQIIAHV 109
RESULT 4	
ADEB64811	
ID	ADEB64811 standard; peptide; 38 AA.
AC	ADEB64811;
XX	
DT	29-JAN-2004 (first entry)
XX	
DE	Corticotropin-releasing factor-2 polypeptide, SEQ ID No 114.
XX	
KW	corticotropin-releasing factor-2; CRF2; myopathic; osteopathic;
KW	hypotensive; cardiant; vasotropic; antimigraine; cerebroprotective;
KW	nootropic; neuroprotective; anorectic; antidiabetic; analgesic;
KW	antiallergic; tranquilizer; anxiolytic; antidepressant; antiarthritic;
XX	gene therapy.
XX	
OS	Unidentified.
XX	

PN WO2003062277-A1.
 PD 31-JUL-2003.
 XX 16-JAN-2003; 2003WO-US001454.
 PF 16-JAN-2002; 2002US-0349117P.
 XX 29-APR-2002; 2002US-0376337P.
 PR 14-JUN-2002; 2002US-0388895P.
 PR 19-SEP-2002; 2002US-0411988P.
 XX (PROC) PROCTER & GAMBLE CO.
 PA Isfort RJ, Mazur WA;
 XX WPI; 2003-787975/74.
 DR New non-native peptide derived from corticotropin-releasing factor-2,
 PT useful for treatment and prevention of e.g. muscular atrophy, also
 PT related nucleic acid and antibodies.
 XX Example 2; SEQ ID NO 114; 304pp; English.
 PS The invention relates to a novel non-native peptide derived from
 XX corticotropin-releasing factor-2 (CRF2). The CRF2 peptides have the
 CC following activities: myopathic, osteopathic, hypotensive, cardiant,
 CC anorectic, antidiabetic, vasotropic, neuroprotective, nootropic,
 CC anxiolytic, antidepressant, analgesic, antiallergic, tranquilizer,
 CC related compounds derived from other proteins. The CRF2 peptides, and
 CC treat disorders modulated by the CRF2 receptor, e.g. skeletal muscle
 CC atrophy or wasting, and bone disorders, however caused; heart/circulatory
 CC diseases (e.g. hypertension, congestive heart failure, heart attack,
 CC reperfusion injury, migraine, stroke, memory loss, Alzheimer's disease,
 CC dementia); joint disorders (osteoarthritis or rheumatoid arthritis);
 CC metabolic disease (obesity or diabetes); pain; allergy; stress; anxiety;
 CC low levels of adrenocorticotrophic hormone; anorexia nervosa; depression;
 CC also to reduce body temperature and to control appetite or cognitive
 CC function. Nucleic acids, optionally labelled, that encode the CRF2
 CC peptides are used as primers and probes for amplification, also for gene
 CC synthesis and for recombinant production of CRF2 peptides, including use
 CC in gene therapy. Antibodies specific for the CRF2 peptides are used to
 CC evaluate expression of the CRF2 peptides after gene therapy. This
 CC sequence represents a novel native CRF polypeptide of the invention.
 XX Sequence 38 AA;
 SQ Query Match 78.2%; Score 140; DB 7; Length 38;
 Best Local Similarity 76.3%; Pred. No. 3.3e-15;
 Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 1 VILSLDVPICGLRILLLEQARYKARNOATNAQILAHV 38
 DB 1 IVLSLDVPICGLRILLLEQARYKARNOATNAQILAHV 38
 RESULT 5
 AD851097
 ID ADE51097 standard; peptide; 38 AA.
 XX ADE51097;
 AC 29-JAN-2004 (first entry)
 XX CRF2 non-native polypeptide, SEQ ID NO 114.
 DE non-native; corticotropin-releasing factor-2; CRF2; myopathic;
 XX osteopathic; hypotensive; cardiant; vasotropic; antidiabetic;
 KW neuroprotective; nootropic; anorectic; analgesic;
 KW anxiolytic; antidepressant; tranquilizer; antiallergic;
 KW antiarthritic.
 XX Unidentified.
 OS

XX WO2003062268-A2.
 PD 31-JUL-2003.
 XX 16-JAN-2003; 2003WO-US001451.
 PF 16-JAN-2002; 2002US-0349117P.
 XX 29-APR-2002; 2002US-0376337P.
 PR 14-JUN-2002; 2002US-0388895P.
 PR 19-SEP-2002; 2002US-0411988P.
 XX (PROC) PROCTER & GAMBLE CO.
 PA Isfort RJ, Mazur WA;
 XX WPI; 2003-787974/74.
 DR New non-native peptide derived from corticotropin-releasing factor-2,
 PT useful for treatment and prevention of e.g. muscular atrophy, also
 PT related nucleic acid and antibodies.
 XX Example 2; SEQ ID NO 114; 300pp; English.
 PS The invention relates to a novel non-native peptide derived from
 XX corticotropin-releasing factor-2 (CRF2). The non-native CRF2 peptides
 CC have the following activities: myopathic, osteopathic, hypotensive,
 CC cardiant, vasotropic, antidiabetic, vasotropic, neuroprotective, nootropic,
 CC anorectic, antidiabetic, vasotropic, neuroprotective, nootropic,
 CC anxiolytic, antidepressant, analgesic, antiallergic, tranquilizer,
 CC related compounds derived from other proteins. The CRF2 peptides, and
 CC treat disorders modulated by the CRF2 receptor, e.g. skeletal muscle
 CC atrophy or wasting, and bone disorders, however caused; heart/circulatory
 CC diseases (e.g. hypertension, congestive heart failure, heart attack,
 CC reperfusion injury, migraine, stroke, memory loss, Alzheimer's disease,
 CC dementia); joint disorders (osteoarthritis or rheumatoid arthritis);
 CC metabolic disease (obesity or diabetes); pain; allergy; stress; anxiety;
 CC low levels of adrenocorticotrophic hormone; anorexia nervosa; depression;
 CC also to reduce body temperature and to control appetite or cognitive
 CC function. Nucleic acids, optionally labelled, that encode the CRF2
 CC peptides are used as primers and probes for amplification, also for gene
 CC synthesis and for recombinant production of CRF2 peptides, including use
 CC in gene therapy. Antibodies specific for the non-native CRF2 peptides are used to
 CC evaluate expression of the non-native CRF2 peptides after gene therapy.
 CC This sequence represents a CRF2 non-native polypeptide of the invention.
 XX Sequence 38 AA;
 SQ Query Match 78.2%; Score 140; DB 7; Length 38;
 Best Local Similarity 76.3%; Pred. No. 3.3e-15;
 Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 1 VILSLDVPICGLRILLLEQARYKARNOATNAQILAHV 38
 DB 1 IVLSLDVPICGLRILLLEQARYKARNOATNAQILAHV 38
 RESULT 6
 AA221009
 ID AA221009 standard; peptide; 38 AA.
 XX AA221009;
 AC 01-JUL-2002 (first entry)
 XX Human urocortin-related peptide (URP).
 DE Human; urocortin-related peptide; URP; antipyrretic; cardiant; urocortin;
 KW ucn; tranquilizer; appetite dysfunction; congestive heart failure;
 KW stress; anxiety.
 XX Homo sapiens.
 OS

XX Key Location/Qualifiers
 FH 38
 FT Modified-site /note= "C-terminal amide"
 FT
 XX
 XX WO200212307-A1.
 XX 14-FEB-2002.
 XX 31-JUL-2001; 2001WO-US023976.
 XX 04-AUG-2000; 2000US-0223255P.
 XX 07-MAR-2001; 2001US-0273969P.
 XX (RERE-) RES DEV FOUND.
 XX Vale WW, Sawchenko PF, Lewis KA, Vaughan JM, Reyes TM, Rivier JE;
 PI Hogenesch JB, Perrin MH;
 XX WPI; 2002-241737/29.
 XX Novel urocortin II polypeptide or human urocortin-related peptide, for
 PT treating high body temperature, appetite dysfunction, congestive heart
 PT failure, stress, anxiety and low levels of adrenocortico tropic hormone.
 XX Claim 36; Fig 4b; 94pp; English.
 XX The invention relates to a modified protein selected from urocortin II
 CC (Ucn II) and human urocortin-related peptide (URP). A pharmaceutical
 CC composition is useful for treating a pathophysiological state including
 CC high body temperature, appetite dysfunction, congestive heart failure,
 CC stress, anxiety and undesirably low levels of adrenocortico tropic
 CC hormone (ACTH) secretions. A modified protein conjugate is useful in
 CC scintigraphy and in various assays, and also for the targeted
 CC destruction of Corticotrophin-releasing factor (CRF) receptor bearing
 CC cells. The present sequence is human URP
 XX Sequence 38 AA;
 Query Match 77.7%; Score 139; DB 5; Length 38;
 Best Local Similarity 76.3%; Pred. No. 4.8e-15;
 Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 1 VILSDVPVIGLLRLLEQARYKAAARNOAATNAQILAHV 38
 Db 1 IVLSLDVPVIGLLQLLEQARARAREQATTNARILARV 38
 RESULT 7
 AAO19442
 ID AAO19442 standard; peptide; 38 AA.
 AC AAO19442;
 XX 10-DEC-2002 (first entry)
 DT Human urocortin-related peptide.
 DE Human; rat; mouse; sheep; cow; chicken; CRF1R; CRP2R;
 KW skeletal muscle atrophy; corticotrophin releasing factor-2 receptor;
 KW muscular dystrophy; corticotrophin releasing factor-1 receptor;
 KW gene therapy.
 XX Homo sapiens.
 OS WO200269908-A2.
 XX 12-SEP-2002.
 XX 06-MAR-2002; 2002WO-US007476.
 XX 06-MAR-2001; 2001US-00799978.
 XX

(PROC) PROCTER & GAMBLE CO.
 XX Isfort RJ, Sheldon RJ;
 XX WPI; 2002-713413/77.
 XX Identifying candidate compounds for regulating skeletal muscle mass or
 PT treating skeletal muscle atrophy by identifying test compounds that bind
 PT to, or activate, the corticotrophin releasing factor-2 receptor.
 XX Disclosure; Page 164; 167pp; English.
 XX The present invention relates to a method of identifying candidate
 CC compounds for regulating skeletal muscle mass or function, and comprises
 CC contacting a test compound with a corticotrophin releasing factor-2
 CC receptor (CRF2R) or with a cell expressing a functional CRF2R,
 CC determining whether the test compound binds to, or activates, the CRF2R
 CC and identifying the test compounds that bind to, or activates, the CRF2R
 CC as candidate compounds for regulating skeletal muscle mass or function.
 CC The method is useful for preparing a medicament for treating skeletal
 CC muscle atrophy or for prophylactic treatment of muscular dystrophies. The
 CC present sequence is a human peptide shown in the invention
 XX Sequence 38 AA;
 Query Match 77.7%; Score 139; DB 5; Length 38;
 Best Local Similarity 76.3%; Pred. No. 4.8e-15;
 Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 1 VILSDVPVIGLLRLLEQARYKAAARNOAATNAQILAHV 38
 Db 1 IVLSLDVPVIGLLQLLEQARARAREQATTNARILARV 38
 RESULT 8
 ABB82356
 ID ABB82356 standard; protein; 38 AA.
 XX ABB82356;
 AC ABB82356;
 XX 08-JAN-2003 (first entry)
 DT Human urocortin II protein (URP) fragment.
 DE Urocortin III; Ucn-III; cardiant; antidiabetic; antimigraine; human;
 KW tranquilliser; antipyretic; vasotropic; gastrointestinal; angiogenic;
 KW vaccine; urocortin II; URP.
 XX Homo sapiens.
 OS WO200274326-A2.
 PN 26-SEP-2002.
 PD 15-MAR-2002; 2002WO-US009115.
 PF 15-MAR-2001; 2001US-0276069P.
 PR 31-MAY-2001; 2001US-0294914P.
 PR (RERE-) RES DEV FOUND.
 PA Vale WW, Rivier JE, Kunitake KS, Lewis KA, Perrin MH, Gulyas J;
 XX WPI; 2002-740838/80.
 XX New human or mouse urocortin III protein, useful e.g. for treating
 PT congestive heart failure, vascular disease, gastrointestinal dysfunction,
 PT diabetes mellitus, high temperature, appetite dysfunction and stress.
 XX Example; Fig 2C; 81pp; English.
 XX The invention relates to an isolated and purified human or mouse
 CC urocortin III (Ucn-III) protein. The Ucn-III protein is useful: (i)

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CC low levels of adrenocorticotrophic hormone; anorexia nervosa; depression;  
CC also to reduce body temperature and to control appetite or cognitive  
CC function. Nucleic acids, optionally labelled, that encode the CRP2  
CC peptides are used as primers and probes for amplification, also for gene  
CC synthesis and for recombinant production of CRF2 peptides, including use  
CC in gene therapy. Antibodies specific for the CRF2 peptides are used to  
CC evaluate expression of the CRF2 peptides after gene therapy. This  
CC sequence represents a novel native CRF polypeptide of the invention.  
XX  
SQ Sequence 38 AA;  
  
Query Match      77.7%; Score 139; DB 7; Length 38;  
Best Local Similarity 76.3%; Pred. No. 4.8e-15;  
Matches 28; Conservative 5; Mismatches 4; Indels 0; Gaps 0  
  
Qy 1 VIIVSLDVPVIGLLRIILLEQARYKARNOQAATNAQILAHV 38  
   :|:|||||||:|||||||:|:|:|:|:|:  
Db 1 IVIIVSLDVPVIGLLQLLLEQARQEAREQATTNARIARV 38  
  
RESULT 10  
ADE64701  
ID ADE644701 standard; peptide; 38 AA.  
XX AC ADE64701;  
XX AC  
XX AC  
DT 29-JAN-2004 (first entry)  
XX DE  
XX CRF-2 related human urocortin II polypeptide, SEQ ID NO 4.  
XX KW corticotropin-releasing factor-2; CRF2; myopathic; osteopathic;  
KW hypotensive; cardiant; vasotropic; antimigraine; cerebroprotective;  
KW neotropic; neuroprotective; anorectic; antidiabetic; analgesic;  
KW anti-allergic; tranquilizer; anxiolytic; antidepressant; antiarthritic;  
KW gene therapy; human.  
XX OS Homo sapiens.  
OS OS  
PN WO2003062277-A1.  
XX PD 31-JUL-2003.  
XX PD  
XX PF 16-JAN-2003; 2003WO-US0001454.  
XX PR 16-JAN-2002; 2002US-0349117P.  
PR 29-APR-2002; 2002US-0376337P.  
PR 14-JUN-2002; 2002US-038895P.  
PR 19-SEP-2002; 2002US-0411988P.  
XX PA (PROC ) PROCTER & GAMBLE CO.  
XX PI Isfort RJ, Mazur WA;  
XX WPI; 2003-787975/74.  
XX DR  
XX PT New non-native peptide derived from corticotropin-releasing factor-2,  
PT useful for treatment and prevention of e.g. muscular atrophy, also  
PT related nucleic acid and antibodies.  
XX PS Example 1; SEQ ID NO 4; 304pp; English.  
XX CC The invention relates to a novel non-native peptide derived from  
CC corticotropin-releasing factor-2 (CRP2). The CRP2 peptides have the  
CC following activities: myopathic, osteopathic, hypotensive, cardiant,  
CC vasotropic, antimigraine, cerebroprotective, neotropic, neuroprotective,  
CC anorectic, antidiabetic, analgesic, antiarthritic, tranquilizer,  
CC anxiolytic, antidepressant, and antiarthritic. The CRP2 peptides, and  
CC related compounds derived from other proteins, are used to prevent or  
CC treat disorders modulated by the CRF2 receptor, e.g. skeletal muscle  
CC atrophy or wasting, and bone disorders, however caused; heart/circulatory  
CC diseases (e.g. hypertension, congestive heart failure, heart attack  
CC reperfusion injury, migraine, stroke, memory loss, Alzheimer's disease,  
CC dementia); joint disorders (osteoarthritis or rheumatoid arthritis);
```

CC	for treating a pathophysiological state including congestive heart
CC	failure, vascular disease, gastrointestinal dysfunction, diabetes
CC	mellitus, high temperature, appetite dysfunction, stress, undesirably low
CC	levels of glucagon secretion or activity, anxiety and migraine headaches; and
CC	(ii) for determining whether a cell has urocortin III receptors; and
CC	(iii) for inhibiting angiogenesis. The present sequence represents the
CC	human urocortin II protein fragment
XX	
SQ	Sequence 38 AA;
	Query Match 77.7%; Score 139; DB 5; Length 38;
	Best Local Similarity 76.3%; Pred. No. 4.8e-15;
	Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY	1 VILSLDVPICLLILLEQARYKKAARNQAATNAQILAHV 38
DB	1 IVLSLDVPICLLILLEQARAAREQATTNARILARV 38
	21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38
RESULT 9	
ID	ADE64820
ID	ADE64820 standard; peptide; 38 AA.
AC	ADE64820;
XX	
AC	ADE64820;
XX	
DT	29-JAN-2004 (first entry)
XX	
DE	Corticotropin-releasing factor-2 polypeptide, SEQ ID NO 123.
XX	
KW	corticotropin-releasing factor-2; CRF2; myopathic; osteopathic;
KW	hypotensive; cardiant; vasotropic; antimigraine; cerebroprotective;
KW	nootropic; neuroprotective; anorectic; antidiabetic; analgesic;
KW	antiallergic; tranquilizer; anxiolytic; antidepressant; antiarthritic;
KW	gene therapy.
XX	
OS	Unidentified.
XX	
XX	WO2003062277-A1.
PN	
XX	
PD	31-JUL-2003.
XX	
PF	16-JAN-2003; 2003WO-US001454.
XX	
XX	16-JAN-2002; 2002US-0349117P.
PR	29-APR-2002; 2002US-0376337P.
PR	14-JUN-2002; 2002US-038895P.
PR	19-SEP-2002; 2002US-0411988P.
XX	
XX	(PROC) PROCTER & GAMBLE CO.
PA	
XX	
PI	Isfort RJ, Mazur WA;
XX	
XX	WPI; 2003-787975/74.
DR	
XX	
PT	New non-native peptide derived from corticotropin-releasing factor-2,
PT	useful for treatment and prevention of e.g. muscular atrophy, also
PT	related nucleic acid and antibodies.
XX	
XX	Example 2; SEQ ID NO 123; 304pp; English.
PS	
XX	
CC	The invention relates to a novel non-native peptide derived from
CC	corticotropin-releasing factor-2 (CRF2). The CRF2 peptides have the
CC	following activities: myopathic, osteopathic, hypotensive, cardiant, and
CC	vasotropic, antimigraine, cerebroprotective, nootropic, neuroprotective,
CC	anorectic, antidiabetic, analgesic, antiallergic, tranquilizer,
CC	anxiolytic, antidepressant, and antiarthritic. The CRF2 peptides, and
CC	related compounds derived from other proteins, are used to prevent or
CC	treat disorders modulated by the CRF2 receptor, e.g. skeletal muscle
CC	atrophy or wasting, and bone disorders, however caused, heart/circulatory
CC	disease (e.g. hypertension, congestive heart failure, heart attack,
CC	reperfusion injury, migraine, stroke, memory loss, Alzheimer's disease,
CC	dementia); joint disorders (osteoarthritis or rheumatoid arthritis);
CC	metabolic disease (obesity or diabetes); pain; allergy; stress; anxiety;

dementia); joint disorders (osteoarthritis or rheumatoid arthritis);
 metabolic disease (obesity or diabetes); pain; allergy; stress; anxiety;
 low levels of adrenocorticotrophic hormone; anorexia nervosa; depression;
 also to reduce body temperature and to control appetite or cognitive
 function. Nucleic acids, optionally labelled, that encode the CR2
 peptides are used as primers and probes for amplification, also for gene
 synthesis and for recombinant production of CR2 peptides, including use
 in gene therapy. Antibodies specific for the CR2 peptides are used to
 evaluate expression of the CR2 peptides after gene therapy. This
 sequence represents a novel native CRF polypeptide of the invention.

Sequence 18 AA:

Query Match 77.7%; Score 139; DB 7; Length 38;
Best Local Similarity 76.3%; Pred. No. 4.8e-15;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 VILSDVPICGLRLLLEOARYKARNQATNAQILAHV 38
: : : : : : : : : : : : : : : : : : :
DB 1 IVLSIDVPIGLLOLILECARARAREOATNARILARV 38

RESULT 12	
ADE51106	
ID	ADE51106 standard; peptide; 38 AA.
XX	
XX	ADE51106;
XX	
XX	
DT	29-JAN-2004 (first entry)
XX	
XX	CRF2 non-native polypeptide, SEQ ID No 123.
DE	
XX	
KW	non-native; corticotropin-releasing factor-2; CRF2; myopathic;
KW	osteopathic; hypotensive; radiant; vasotropic; antimigraine;
KW	cardioprotective; nootropic; neuroprotective; anorectic; antidiabetic;
KW	analgesic; antiallergic; tranquilizer; anxiolytic; antidepressant;
KW	antiarthritic.

XX OS Unidentified.
XX PN WO2003062268-A2.
XX PD 31-JUN-2003

XX	16-JAN-2003; 2003WO-US001451.
PF	
XX	
PR	16-JAN-2002; 2002US-0349117P.
PR	29-APR-2002; 2002US-0376337P.
PR	14-JUN-2002; 2002US-0389895P.
PR	19-SEP-2002; 2002US-0411988P.
XX	

XX Isfort RJ, Mazur WA;
PI
XX
XX
DE WPI; 2003-787974/74.
XX
XX New non-native peptide derived from corticotropin-releasing factor-2
PT useful for treatment and prevention of e.g. muscular atrophy, also
PT plasma, nucleic acid and antibodies.
PT

XX
PS Example 2; SEQ ID NO 123; 300pp; English.
XX
CC The invention relates to a novel non-native peptide derived from
CC corticotropin-releasing factor-2 (CRF2). The non-native CRF2 peptides
CC have the following activities: myopathic, osteopathic, hypotensive,
CC diuretic, vasotropic, antimigraine, cerebroprotective, hypnotic,
CC neuroprotective, anorectic, antidiabetic, analgesic, anti-allergic,
CC tranquilizer, anxiolytic, antidepressant, and antiarrhythmic. The non-
CC native CRF2 peptides, and related compounds derived from other proteins
CC e.g. skeletal muscle atrophy or wasting, and bone disorders, however
CC caused, heart/circulatory diseases (e.g. hypertension, congestive heart

The invention relates to a novel non-native peptide derived from corticotropin-releasing factor-2 (CRF2). The non-native CRF2 peptides have the following activities: myopathic, osteopathic, hypotensive, cardiac, vasotropic, antimigraine, cerebroprotective, nootropic, neuroprotective, anorectic, antidiabetic, analgesic, antiallergic, tranquiliser, anxiolytic, antidepressant, and antiarthritic. The non-native CRF2 peptides, and related compounds derived from other proteins are used to prevent or treat disorders modulated by the CRF2 receptor.

xx The invention relates to a novel non-native peptide derived from
cc corticotropin-releasing factor-2 (CRF2). The non-native CRF2 peptides
cc have the following activities: myopathic, osteopathic, hypotensive,
cc cardiant, vasotropic, antimigraine, cerebroprotective, neurotropic,
cc neuroprotective, anorectic, antidiabetic, analgesic, antiallergic,
cc tranquilizer, anxiolytic, antidepressant, and antiarthritis; the non-

vasotropic, antimigraine, cerebroprotective, nootropic, neuroprotective, anorectic, antidiabetic, analgesic, antiallergic, tranquilizer, anxiolytic, antidepressant, and antiarthritic. The CRF2 peptides, and related compounds derived from other proteins, are used to prevent or treat disorders modulated by the CRF2 receptor, e.g. skeletal muscle atrophy or wasting, and bone disorders, however caused; heart/circulatory diseases (e.g. hypertension, congestive heart failure, heart attack, reperfusion injury, migraine, stroke, memory loss, Alzheimer's disease, dementia); joint disorders (osteoarthritis or rheumatoid arthritis); metabolic disease (obesity or diabetes); pain; allergy; stress; anxiety; low levels of adrenocorticotrophic hormone; anorexia nervosa; depression; also to reduce body temperature and to control appetite or cognitive function. Nucleic acids, optionally labelled, that encode the CRF2 peptides are used as primers and probes for amplification, also for gene synthesis and for recombinant production of CRF2 peptides, including use in gene therapy. Antibodies specific for the CRF2 peptides are used to evaluate expression of the CRF2 peptides after gene therapy. This sequence represents a novel native CRF polypeptide of the invention.

XX
SQ Sequence 39 AA;

Query Match 77.7%; Score 139; DB 7; Length 39;
Best Local Similarity 76.3%; Pred. NO. 5e-15;
Matches 29; Conservative 5; Mismatches 4; Indels

QY		1 VIIISLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
	:	::::: :
	:	::::: :
D6	1 VIIISLDVPIGLLOITILECARAAREOATTNARILARY 38	
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	:	::::: :

Search completed: April 20, 2004, 18:54:43

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Search completed: April 20, 2004, 18:54:43
Job time : 25.3333 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 20, 2004, 18:53:13 ; Search time 8.36 Seconds
(without alignments)
234.664 Million cell updates/sec

Title: US-09-919-473-11
Perfect score: 179
Sequence: 1 VILSDVPILGLRILLLEQARYKAARNQAATNAQILAHV 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents RA: *
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2: /cgn2_6/prodata/2/iaa/5B-COMB.pcp:*
3: /cgn2_6/prodata/2/iaa/6A-COMB.pcp:*
4: /cgn2_6/prodata/2/iaa/6B-COMB.pcp:*
5: /cgn2_6/prodata/2/iaa/PCTUS-COMB.pcp:*
6: /cgn2_6/prodata/2/iaa/backfiles1.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	179	100.0	38	4	US-09-799-978-43
2	139	77.7	38	4	US-09-799-978-44
3	63	35.2	41	4	US-09-799-978-45
4	61	34.1	41	1	US-07-709-091-8
5	61	34.1	41	1	US-08-104-862-8
6	61	34.1	41	1	US-08-865-773-9
7	61	34.1	41	3	US-08-981-189B-4
8	61	34.1	41	4	US-09-400-716-6
9	61	34.1	41	4	US-09-400-716-7
10	61	34.1	41	4	US-09-424-127-9
11	61	34.1	41	6	5177060-6
12	60	33.5	40	3	US-08-981-189B-8
13	60	33.5	40	4	US-09-400-716-10
14	60	33.5	40	4	US-09-400-716-11
15	60	33.5	40	4	US-09-356-139-3
16	60	33.5	41	1	US-08-865-773-8
17	60	33.5	41	3	US-08-981-189B-5
18	60	33.5	41	3	US-08-981-189B-17
19	60	33.5	41	4	US-09-424-127-8
20	60	33.5	41	6	5177060-7
21	60	33.5	124	3	US-08-981-189B-15
22	58	32.4	41	1	US-07-709-091-3
23	58	32.4	41	1	US-07-715-752A-3
24	58	32.4	41	1	US-08-104-862-3
25	58	32.4	41	1	US-08-162-178-3
26	58	32.4	41	1	US-08-865-773-4
27	58	32.4	41	4	US-09-424-127-4

28	58	32.4	41	5	PCT-US92-05101-3
29	57	31.8	41	1	US-07-709-091-2
30	57	31.8	41	1	US-07-715-752A-2
31	57	31.8	41	1	US-08-104-862-2
32	57	31.8	41	1	US-08-162-178-2
33	57	31.8	41	1	US-08-480-756-7
34	57	31.8	41	1	US-08-865-773-2
35	57	31.8	41	1	US-08-865-773-5
36	57	31.8	41	3	US-08-981-189B-3
37	57	31.8	41	3	US-09-400-716-1
38	57	31.8	41	4	US-09-400-716-2
39	57	31.8	41	4	US-09-424-127-2
40	57	31.8	41	4	US-09-424-127-5
41	57	31.8	41	4	US-09-356-139-1
42	57	31.8	41	4	US-09-356-139-1
43	57	31.8	41	5	PCT-US92-05101-2
44	57	31.8	41	6	5177060-1
45	57	31.8	41	6	5177060-2

ALIGNMENTS

RESULT 1
US-09-799-978-43
; Sequence 43, Application US/09799978
; Patent No. 6670140

; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or Function Using Corticotropin Releasing Factor Receptors
; FILE REFERENCE: 8448
; CURRENT APPLICATION NUMBER: US/09/799,978
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 43
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-799-978-43

Query Match 100.0%; Score 179; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 3.2e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VILSDVPILGLRILLLEQARYKAARNQAATNAQILAHV 38
Db 1 VILSDVPILGLRILLLEQARYKAARNQAATNAQILAHV 38

RESULT 2
US-09-799-978-44
; Sequence 44, Application US/09799978
; Patent No. 6670140

; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or Function Using Corticotropin Releasing Factor Receptors
; FILE REFERENCE: 8448
; CURRENT APPLICATION NUMBER: US/09/799,978
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 44
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-978-44

REGISTRATION NUMBER: 20856

[illegible]

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[illegible]

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Db      6 ISLDITFHLRLVLEMARAEQLAQAHNRK1MA 39

RESULT 6
US-08-865-773-9
; Sequence 9, Application US/08865773
; Patent No. 5777073
; GENERAL INFORMATION:
; APPLICANT: RIVIER, Jean E.F.
; TITLE OF INVENTION: CYCLIC CRF ANTAGONIST PEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FITCH, EVEN, TABIN & FLANNERY
; STREET: 135 S. LaSalle Street, Suite 900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,773
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/556,578
; FILING DATE: 13-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/353,928
; FILING DATE: 12-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Schumann, James J.
; REGISTRATION NUMBER: 20,856
; REFERENCE/DOCKET NUMBER: 57670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-552-1311
; TELEFAX: 619-552-0095
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-865-773-9

Query Match      34.1%; Score 61; DB 1; Length 41;
Best Local Similarity 38.9%; Pred. No. 0.013;
Matches 14; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

Qy      3 LSDDVPGLRLLEQARYKAARNQAATNAQILAHV 38
Db      6 ISIDLTFHLRLNMIEMARIENEREQAGLNKRYLDEV 41

RESULT 7
US-08-981-189B-4
; Sequence 4, Application US/08981189B
; Patent No. 6214797
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: UROCORTIN PEPTIDES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FITCH, EVEN, TABIN & FLANNERY
; STREET: 120 S. LaSalle Street, Suite 1600
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,189B
; FILING DATE: 10-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,144
; FILING DATE: 13-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/002,223
; FILING DATE: 11-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Schumann, James J.
; REGISTRATION NUMBER: 20,856
; REFERENCE/DOCKET NUMBER: 57611
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-552-1311
; TELEFAX: 858-552-0095
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-981-189B-4

Query Match      34.1%; Score 61; DB 3; Length 41;
Best Local Similarity 38.9%; Pred. No. 0.013;
Matches 14; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

Qy      3 LSDDVPGLRLLEQARYKAARNQAATNAQILAHV 38
Db      6 ISIDLTFHLRLNMIEMARIENEREQAGLNKRYLDEV 41

RESULT 8
US-09-400-716-6
; Sequence 6, Application US/09400716
; Patent No. 6319900
; GENERAL INFORMATION:
; APPLICANT: Wei, Edward T.
; TITLE OF INVENTION: INHIBITION OF ABNORMAL CELL GROWTH WITH
; TITLE OF INVENTION: CORTICOTROPIN-RELEASING HORMONE ANALOGS
; FILE REFERENCE: 2900 006USO
; CURRENT APPLICATION NUMBER: US/09/400,716
; CURRENT FILING DATE: 1999-09-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Sucker fish
US-09-400-716-6

Query Match      34.1%; Score 61; DB 4; Length 41;
Best Local Similarity 38.9%; Pred. No. 0.013;
Matches 14; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

Qy      3 LSDDVPGLRLLEQARYKAARNQAATNAQILAHV 38
Db      6 ISIDLTFHLRLNMIEMARIENEREQAGLNKRYLDEV 41

RESULT 9
US-09-400-716-7
; Sequence 7, Application US/09400716
; Patent No. 6319900
; GENERAL INFORMATION:
; APPLICANT: Wei, Edward T.
; TITLE OF INVENTION: INHIBITION OF ABNORMAL CELL GROWTH WITH

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;; TITLE OF INVENTION: CORTICOTROPIN-RELEASING HORMONE ANALOGS
;; FILE REFERENCE: 2900.006USO
;; CURRENT APPLICATION NUMBER: US/09/400,716
;; CURRENT FILING DATE: 1999-09-21
;; NUMBER OF SEQ ID NOS: 12
;; SOFTWARE: Patent In Ver. 2.1
;; SEQ ID NO 7
;; LENGTH: 41
;; TYPE: PRT
;; ORGANISM: Carp
US-09-400-716-7

Query Match 34.1%; Score 61; DB 4; Length 41;
Best Local Similarity 38.9%; Pred. No. 0.013;
Matches 14; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 3 LSLDVPGLRLLEQARYKAARNQAATNAQILAHV 38
Db 6 ISIDLTFHLRNMIENIARIENEREQAQLNRKYLDEV 41

RESULT 10

US-09-424-127-9
; Sequence 9, Application US/09424127
; Patent No. 6323312
; GENERAL INFORMATION:
; APPLICANT: RIVIER, Jean E.F.
; TITLE OF INVENTION: CYCLIC CRF ANTAGONIST PEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FITCH, EVEN, TABIN & FLANNERY
; STREET: 135 S. LaSalle Street, Suite 900
; City: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/424,127
; FILING DATE: 17-NOV-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/865,773
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Schumann, James J.
; REGISTRATION NUMBER: 20,856
; REFERENCE/DOCKET NUMBER: 57670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-552-1311
; TELEFAX: 619-552-0095
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; LENGTH: 41 amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-424-127-9

Query Match 34.1%; Score 61; DB 4; Length 41;
Best Local Similarity 38.9%; Pred. No. 0.013;
Matches 14; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 3 LSLDVPGLRLLEQARYKAARNQAATNAQILAHV 38
Db 6 ISIDLTFHLRNMIENIARIENEREQAQLNRKYLDEV 41

RESULT 11

5177060-6
; Patent No. 5177060
; APPLICANT: WEI, EDWARD T.
; TITLE OF INVENTION: ANTI-INFLAMMATORY PEPTIDES AND TREATMENT
; TO INHIBIT VASCULAR LEAKAGE IN INJURED TISSUES
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,578
; FILING DATE: 09-JAN-1990
; SEQ ID NO:6:
; LENGTH: 41
5177060-6

Query Match 34.1%; Score 61; DB 6; Length 41;
Best Local Similarity 38.9%; Pred. No. 0.013;
Matches 14; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 3 LSLDVPGLRLLEQARYKAARNQAATNAQILAHV 38
Db 6 ISIDLTFHLRNMIENIARIENEREQAQLNRKYLDEV 41

RESULT 12

US-08-981-189B-8
; Sequence 8, Application US/08981189B
; Patent No. 6214797
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: UROCORTIN PEPTIDES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FITCH, EVEN, TABIN & FLANNERY
; STREET: 120 S. LaSalle Street, Suite 1600
; City: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,189B
; FILING DATE: 10-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,144
; FILING DATE: 13-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/002,223
; FILING DATE: 11-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Schumann, James J.
; REGISTRATION NUMBER: 20,856
; REFERENCE/DOCKET NUMBER: 57611
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-552-1311
; TELEFAX: 858-552-0095
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-981-189B-8

Query Match 33.5%; Score 60; DB 3; Length 40;
Best Local Similarity 44.4%; Pred. No. 0.018;
Matches 16; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 3 LSLDVPGLRLLEQARYKAARNQAATNAQILAHV 38
Db 5 ISIDLTFHLRLLELARTSQERAEQNRIIFDSV 40

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; EARLIER APPLICATION NUMBER: 08/504,856
; EARLIER FILING DATE: 1995-07-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-356-139-3

Query Match      33.5%; Score 60; DB 4; Length 40;
Best Local Similarity 44.4%; Pred. No. 0.018;
Matches 16; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

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Db      5 LSLDTFHLRLTLELARTSQQRERAEQNRIIFDSV 40
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Job time : 9.36 secs

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RESULT 13
US-09-400-716-10
; Sequence 10, Application US/09400716
; Patent No. 6319900
; GENERAL INFORMATION:
; APPLICANT: Wei, Edward T.
; APPLICANT: Slominski, Andrzej T.
; TITLE OF INVENTION: INHIBITION OF ABNORMAL CELL GROWTH WITH
; TITLE OF INVENTION: CORTICOTROPIN-RELEASING HORMONE ANALOGS
; FILE REFERENCE: 2900.006USO
; CURRENT APPLICATION NUMBER: US/09/400,716
; CURRENT FILING DATE: 1999-09-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 10
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Rat
US-09-400-716-10

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Query Match      33.5%; Score 60; DB 4; Length 40;
Best Local Similarity 44.4%; Pred. No. 0.018;
Matches 16; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY      3 LSLDVPICGLRLLLEQARYKARNQAATNAQILAHV 38
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Db      5 LSLDTFHLRLTLELARTSQQRERAEQNRIIFDSV 40
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RESULT 14
US-09-400-716-11
; Sequence 11, Application US/09400716
; Patent No. 6319900
; GENERAL INFORMATION:
; APPLICANT: Wei, Edward T.
; APPLICANT: Slominski, Andrzej T.
; TITLE OF INVENTION: INHIBITION OF ABNORMAL CELL GROWTH WITH
; TITLE OF INVENTION: CORTICOTROPIN-RELEASING HORMONE ANALOGS
; FILE REFERENCE: 2900.006USO
; CURRENT APPLICATION NUMBER: US/09/400,716
; CURRENT FILING DATE: 1999-09-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 11
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Human
US-09-400-716-11

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Query Match      33.5%; Score 60; DB 4; Length 40;
Best Local Similarity 44.4%; Pred. No. 0.018;
Matches 16; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY      3 LSLDVPICGLRLLLEQARYKARNQAATNAQILAHV 38
      |||:|||||:|||||:|||||:|||||:|||||:
Db      5 LSLDTFHLRLTLELARTSQQRERAEQNRIIFDSV 40
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RESULT 15
US-09-356-139-3
; Sequence 3, Application US/09356139
; Patent No. 6680367
; GENERAL INFORMATION:
; APPLICANT: Desjardins, Clarissa
; TITLE OF INVENTION: FLUORESCENT CRF RECEPTOR-BINDING
; TITLE OF INVENTION: PEPTIDES
; FILE REFERENCE: 06942/022001
; CURRENT APPLICATION NUMBER: US/09/356,139
; CURRENT FILING DATE: 1999-07-19
; EARLIER APPLICATION NUMBER: 08/682,810
; EARLIER FILING DATE: 1996-07-10

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 20, 2004, 18:56:48 ; Search time 19.5067 Seconds
(without alignments)
537.026 Million cell updates/sec

Title: US-09-919-473-11

Perfect score: 179

Sequence: 1 VILSLDVPGLRILLEQARYKAARNOATNAQILAHV 38

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Gapop 10.0 , Gapext 0.5

Searched: 1124875 seqs, 275673149 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	179	100.0	38	9	US-09-919-473-11
2	179	100.0	38	10	US-09-799-978-43
3	179	100.0	38	14	US-10-099-766-9
4	179	100.0	112	9	US-09-919-473-10
5	140	78.2	38	14	US-10-315-964A-114
6	140	78.2	38	14	US-10-317-251A-114
7	140	78.2	38	14	US-10-317-252A-114
8	139	77.7	38	9	US-09-919-473-4
9	139	77.7	38	10	US-09-799-978-44
10	139	77.7	38	14	US-10-099-766-8
11	139	77.7	38	14	US-10-315-964A-4
12	139	77.7	38	14	US-10-315-964A-123
13	139	77.7	38	14	US-10-315-964A-354
14	139	77.7	38	14	US-10-317-251A-4
15	139	77.7	38	14	US-10-317-251A-123

16	139	77.7	38	14	US-10-317-251A-354
17	139	77.7	38	14	US-10-317-252A-4
18	139	77.7	38	14	US-10-317-252A-123
19	139	77.7	38	14	US-10-317-252A-354
20	139	77.7	39	14	US-10-315-964A-356
21	139	77.7	39	14	US-10-315-964A-368
22	139	77.7	39	14	US-10-317-251A-356
23	139	77.7	39	14	US-10-317-251A-368
24	139	77.7	39	14	US-10-317-252A-356
25	139	77.7	39	14	US-10-317-252A-368
26	139	77.7	41	9	US-09-919-473-3
27	139	77.7	112	9	US-09-682-706-2
28	139	77.7	112	9	US-09-919-473-2
29	138	77.1	38	14	US-10-315-964A-122
30	138	77.1	38	14	US-10-317-251A-122
31	138	77.1	38	14	US-10-317-252A-122
32	137	76.5	38	14	US-10-315-964A-110
33	137	76.5	38	14	US-10-317-251A-110
34	137	76.5	38	14	US-10-317-252A-110
35	136	76.0	38	14	US-10-315-964A-109
36	136	76.0	38	14	US-10-315-964A-124
37	136	76.0	38	14	US-10-315-964A-127
38	136	76.0	38	14	US-10-315-964A-130
39	136	76.0	38	14	US-10-317-251A-109
40	136	76.0	38	14	US-10-317-251A-124
41	136	76.0	38	14	US-10-317-251A-127
42	136	76.0	38	14	US-10-317-251A-130
43	136	76.0	38	14	US-10-317-252A-109
44	136	76.0	38	14	US-10-317-252A-124
45	136	76.0	38	14	US-10-317-252A-127

ALIGNMENTS

RESULT 1
US-09-919-473-11
; Sequence 11, Application US/09919473
; Patent No. US20020127221A1
; GENERAL INFORMATION:
; APPLICANT: Vale, Wylie Walker Jr.
; APPLICANT: Lewis, Kathy Ann
; APPLICANT: Reyes, Teresa Marie
; APPLICANT: Hogenesch, John Beren
; APPLICANT: Sawchenko, Paul Emil
; APPLICANT: Vaughan, Joan Maureen
; APPLICANT: Rivier, Jean Edouard Frederic
; APPLICANT: Perrin, Marilyn Heller
; TITLE OF INVENTION: Urocortin Proteins and Uses Thereof
; FILE REFERENCE: D6334
; CURRENT APPLICATION NUMBER: US/09/919,473
; CURRENT FILING DATE: 2001-07-31
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 11
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: Mouse Urocortin II
US-09-919-473-11

Query Match 100.0%; Score 179; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.6e-20;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VILSLDVPGLRILLEQARYKAARNOATNAQILAHV 38
DB 1 VILSLDVPGLRILLEQARYKAARNOATNAQILAHV 38

RESULT 2

Matches 29; Conservative 5; Mismatches 4; Indels 0

QY	1	VILSLDVPILGLRILLQARYKARNQAAATWQILAHV	38
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DB	1	IVLSLDPVIGLQLLQARQARAREATTNARILARY	38
	:		

RESULT 6
US-10-317-251A-114

RESULT 7
US-10-317-252A-114
Sequence 114, Application US/10317252A
Publication No. US20030148958A1
GENERAL INFORMATION:
APPLICANT: The Procter & Gamble Company
APPLICANT: Isfort, Robert J
APPLICANT: Mazur, Wieslaw A
TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists
FILE REFERENCE: 8847M
CURRENT APPLICATION NUMBER: US/10/317,252A
CURRENT FILING DATE: 2003-03-31
PRIORITY APPLICATION NUMBER: US 60/349,117
PRIORITY FILING DATE: 2002-01-16
PRIORITY APPLICATION NUMBER: US 60/376,337
PRIORITY FILING DATE: 2003-04-29
PRIORITY APPLICATION NUMBER: US 60/388,895
PRIORITY FILING DATE: 2002-06-14
PRIORITY APPLICATION NUMBER: US 60/411,988
PRIORITY FILING DATE: 2003-09-19
NUMBER OF SEQ ID NOS: 530
SOFTWARE: PatentIn version 3.2
SEQ ID NO 114
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Chemically synthesized artificial peptide
FEATURE:
NAME/KEY: MOD RES
LOCATION: (38)..(38)
OTHER INFORMATION: AMIDATION

Query Match 77.7%; Score 139; DB 10; Length 38;
Best Local Similarity 76.3%; Pred. No. 4.2e-14;
Matches 29; Conservative 5; Mismatches 4; Indels

Query Match 77.7%; Score 139; DB 14; Length 38;
Best Local Similarity 76.3%; Pred. No. 4.2e-14;
Matches 29; Conservative 5; Mismatches 4; Indels

RESULT 13
US-10-315-964A-354
; Sequence 354, Application US/10315964A
; Publication No. US20030148956A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert J
; APPLICANT: Mazur, Wieslaw A
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists
; FILE REFERENCE: 8847M3
; CURRENT APPLICATION NUMBER: US/10/315,964A
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US 60/349,117
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/376,337
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/388,895
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/411,988
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 530
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 354
; LENGTH: 38


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1 TYPE: PRT
2
3 ORGANISM: Artificial
4
5 FEATURE:
6
7 FEATURE:
8 NAME/KEY: MOD_RES
9 LOCATION: (1)..(1)
10 OTHER INFORMATION: ACETYLATION
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12 FEATURE:
13 NAME/KEY: MOD_RES
14 LOCATION: (38)..(38)
15
16 OTHER INFORMATION: AMIDATION
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18 US-10-115-964A-354

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RESULT 14
US-10-317-251A-4
; Sequence 4, Application US/10317251A
; Publication No. US20030148957A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert J
; APPLICANT: Mazur, Wieslaw A
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists
; FILE REFERENCE: 8847M2
; CURRENT APPLICATION NUMBER: US/10/317,251A
; CURRENT FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: US 60/349,117
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/376,337
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/388,895
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/411,988
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 530
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-317-251A-4

Query Match	77.7%	Score 139;	DB 14;	Length 38;
Best Local Similarity	76.3%	Pred. No. 4.2e-14;		
Matches 29; Conservative	5;	Mismatches 4;	Indels 0;	Gaps 0;
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Dh	1	IVLSIDVPIGLIOLLEQARAPAREQATTNARILARY	38	

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US-10-317-251A-123
; Sequence 123, Application US/10317251A
; Publication No. US20030148957A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert J
; APPLICANT: Mazur, Wieslaw A
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists
; FILE REFERENCE: 8847M2
; CURRENT APPLICATION NUMBER: US/10/317,251A
; CURRENT FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: US 60/349,117

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, PRIOR FILING DATE: 2002-01-16
, PRIOR APPLICATION NUMBER: US 60/376,337
, PRIOR FILING DATE: 2002-04-29
, PRIOR APPLICATION NUMBER: US 60/388,895
, PRIOR FILING DATE: 2002-06-14
, PRIOR APPLICATION NUMBER: US 60/411,988
, PRIOR FILING DATE: 2003-09-19
, NUMBER OF SEQ ID NOS: 530
, SOFTWARE: PatentIn version 3.2
, SEQ ID NO 123
, LENGTH: 39
, TYPE: PRT
, ORGANISM: Artificial
, FEATURE:
, OTHER INFORMATION: Chemically synthesized artificial peptide
, FEATURE:
, NAME/KEY: MOD RES
, LOCATION: (38)..(38)
, OTHER INFORMATION: AMIDATION
, US-10-317-251A-123

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Query Match          77.8%; Score 139; DB 14; Length 38;
Best Local Similarity 76.3%; Pred.No. 4.2E-14;
Matches 29; Conservative 5; Mismatches 4; Indels
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